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RESULT 1
AAM48000
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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Arabidopsis CDPK2	Arabidopsis thalia	Arabidopsis CDPK4	Arabidopsis thalia	Soybean CDPK prote	Arabidopsis thalia	Arabidopsis thalia	Arabidopsis, thalia	ý.	Arabidopsis thalia
SUMMARIES	AAM48000	AAG35776	AAM48001				AAG31158	AAG31157	AAG38599	AAG38598
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Lengt	4	20	50	42	51	39	483	55	85	8
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ALIGNMENTS

Arabidopsis; CDPK2; CDPK4; calcium dependent protein kinase; oilseed; disease resistance; agricultural; pathogen; crop yield; ornamental; fungicide; bactericide; nematocide; insecticide; viricide; cereal; transgenic; plant; enzyme. AAM48000 standard; Protein; 495 AA. Arabidopsis CDPK2 SEQ ID NO 1. 04-MAY-2001; 2001WO-US14368. 05-MAY-2000; 2000US-201925P. 08-MAR-2002 (first entry) (GEHO) GEN HOSPITAL CORP. Arabidopsis thaliana. WPI; 2002-062179/08. N-PSDB; ABA06021 WO200184911-A1. 15-NOV-2001. AAM48000; Sheen J;

Producing plant having increased disease resistance, comprises

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regenerating plant from a non-naturally occurring plant cell
over-expressing a polynucleotide encoding a calcium dependent protein
kinase polypeptide
                      Disclosure, Fig 1; 44pp; English.
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Matches 495; Conservative
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16-APR-1999;
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23-APR-1999;
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14-MAY-1999;
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18-MAY-1999;
19-MAY-1999;
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24-MAY-1999;
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06-APR-1999;
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                                                                              AAG35776;
RESULT 2
                      AAG35776
                                                                              The invention relates to producing a plant having increased disease resistance, comprising providing a non-naturally occurring plant cell cover-expressing a polymucleotide encoding a calcium dependent protein kinase (CDFK) polypeptide and regenerating a plant from the plant call, where the CDPK polypeptide is expressed in the plant, increasing the plant to disease as compared to a contract call, where the CDPK polypeptide is expressed in the plant, increasing the plant of the plant to disease as compared to a contract c
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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter;
                                                                                       Arabidopsis thaliana protein fragment SEQ ID NO: 43753.
AAG35776 standard; Protein; 501 AA.
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99US-0123180.
99US-0123180.
99US-0125788.
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99US-0139456

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99US-0139459.
99US-0139459.
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99US-01394610.
99US-01394610.
99US-01394610.
99US-0139462.
99US-0139750.
99US-0140353.
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CREDYEDUWREIQIMEHLSEHPNUVRIKGTYEDSVFUHIVMEVCEGGELFDRIVSKGHFS 123 EREAVKLIKTILGVVEACHSLGVMHRDLKPENFLFDSPKDDAKLKATDFGLSVFYKPGQY CREDYEDVWREIQIMEHLSEHPNVVRIKGIYEDSVFVHIVMEVCEGGELFDRIVSKGCFS EREAAKLIKTILGVVEACHSLGVOHRDLKPENFLFDSPSDDAKLKATDFGLSVFYKPGQY 4 , Length 501; Indels 94.8%; Score 2458; DB 21; 94.8%; Pred. No. 2.2e-210; ive 9; Mismatches 13; 9905-0149723.
9905-0149929.
9905-0149929.
9905-0149930.
9905-0149930.
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9905-0151080. Query Match
Best Local Similarity 94.8
Matches 470, Conservative 20-AUG-1999; 23-AUG-1999; 23-AUG-1999; 23-AUG-1999; 27-AUG-1999; 27-AUG-1999; 27-AUG-1999; 30-AUG-1999; 30-AUG-1999; 31-AUG-1999; 31-AU 4 m 64 63 124 임 ò $\dot{\delta}$

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Gaps

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Producing plant having increased disease resistance, comprises regenerating plant from a non-naturally occurring plant cell over-expressing a polynucleotide encoding a calcium dependent protein
                                                                                                                                                                                                                                                                                                                                                                                                                               Arabidopsis, CDPK2, CDPK4, calcium dependent protein kinase, oilseed, disease resistance, agricultural, pathogen, crop yield, ornamental, fungicide, bactericide, nematocide, insecticide, viricide, cereal;
                                                                                               363
                                                                                                                                             423
                                                                                                                                                              MESEIKSLMDAADIDNSGTIDYGEFLAATLHINKMEREENLVVAFSYFDKDGSGYITIDE 422
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                                                                     302
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LYDVVGSPYYVAPEVLKKCYGPEIDVWSAGVILYILLSGVPPFWAETESGIFRQILQGKL
                  183 LYDVVGSPYYVAPBVLKKCYGPEIDVWSAGVILYILLSGVPPFWAETESGIFRQILQCKI
                                              DEKSDPWPTISEAAKDLIYKMLERSPKKRISAHEALCHPWIVDEQAAPDKPLDPAVLSRL
                                                                       243 DEKSDEWPTISEGAKDLIYKMLDRSPKKRISAHEALCHPWIVDEHAAPDKPLDPAVLSRL
                                                                                               KOFSOMNKIKKMALRVIAERLSEEIGGLKELFKMIDTDNSGTITFEELKAGLKRVGSEL
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                                                                                                                                                                                                                                                                                                                                                                                                          Arabidopsis CDPK4 SEQ ID NO 3.
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EAFGVEDTSSTAKSDD 498
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The invention relates to producing a plant having increased disease resistance, comprising providing a non-naturally occurring plant cell over-expressing a polyuncleotide encoding a calcium dependent protein kinase (CDPK) polypeptide and regenerating a plant from the plant cell, where the CDPK polypeptide is expressed in the plant, increasing the resistance of the plant to disease as compared to a plant increasing naturally-occurring plant. The method is useful for a variety of agricultural and commercial purposes including improving a plant's

Disclosure, Fig 2, 44pp, English.

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crosstance against plant pathogens, increasing crop yields, improving crop and ornamental quality and reducing agricultural production costs.

The method facilitates an effective and economical method for in-plant protection against plant pathogen, reducing or minimising the need for traditional chemical practices (e.g. application of fungicides, conficiency insecticides, or viricides) that are typically used by farmers for controlling the spread of plant pathogens and providing protection against disease causing pathogens. The method contributes to the production of high quality and high yield agricultural providing protects, e.g. fruits, ornamentals, vegetables, cereals and field crops pathogens, agricultural products with increased shelf-life and reduced handling costs and high quality and yield crops for agricultural (e.g. cereal and field crops), industrial (e.g. oilseeds) and commercial (e.g. cereal and field crops), industrial (e.g. oilseeds) and commercial (e.g. fiber crops) purposes. The present sequence is that of Abrabidopsis thaliana CDPK4 of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  243 DFKSDPWPTISEGAKDLIYKMLDRSFKKRISAHEALCHPWIVDEHAAPDKPLDPAVLSRL 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   303 KOFSOMNKIKKMALKVIAERLSEBIGGLKELFKMIDTDNSCTITFEELKAGLKRVGSEL 362
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             363 MESEIKSLMDAADIDNSGTIDYGEFLAATLHINKMEREENLVVAFSYFDKDGSGYITIDE 422
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     63 CREDYEDVWREIQIMHHLSEHPNVVRIKGTYEDSVFVHIVMEVCEGGELFDRIVSKGCFS 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 KPNPRRPSNTVLPYQTPRLRDHYLLGKKLGQGGGFGTTYLCTEKSTSANYACKSIPKRKLV 63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         244 DFKSDPWPTISEAAKDLIYKMLERSPKKRISAHBALCHPWIVDEQAAPDKPLDPAVLSRL
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                                                                                                                                                                                                                                                                                                                                                                                                                     Length 501;
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Pred. No. 2.2e-210;
9; Mismatches 13;
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Best Local Similarity 94.8
Matches 470; Conservative
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              Arabidopsis thaliana
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17-MAY-1999;

18-MAY-1999;

18-MAY-1999;
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                                   EP1033405-A2
                                                          06-SEP-2000
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This invention describes a novel nucleic acid molecule and its encoded protein that are induced upon pathogen invasion or elicitor treatment. The products of the invention are functional in plants, plant tissue and in plant cells for inducible gene expression and altering the disease resistance phenotype of plants. The products of the invention are related to calcium dependent protein kinase (CDPK) genes. The invention describes the isolation of a novel tobacco CDPK protein fragment and its encoding nucleic acid, isolated from a cell suspension culture derived from a tobacco cultivar KT14 explant, after growth in the presence of the elicitin paramiticein. This sequence represents the soybean CDPK protein which is used in the description of the method.
                                                                                                                                                                                                                                                 CDPK, calcium dependent protein kinase; tobacco; pathogen; invasion; induction; elicitor; plant; disease resistance; parasiticein; soybean; elicitin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New polynucleotides based on calcium dependent protein kinase genes - useful to induce disease resistance in plants
1..46
note= "protein kinase seguence"
                                                                                                                                                                                                                                                                                                                                                                                                                    'note= "protein kinase sequence"
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/note= "calcium binding site"
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/note= "calcium binding site"
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/note= "p
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               138 VEACHSLGVMHRDLKPENFLFDSPKDDAKLKATDFGLSVFYKPGQYLYDVVGSPYYVAPE 197
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99US-0160980.
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19-MAY-1999)
20-MAY-1999
21-MAY-1999
24-MAY-1999
25-MAY-1999
26-MAY-1999
01-JUN-1999
04-JUN-1999
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16-70N-1999;
17-70N-1999;
18-70N-1999;
18-70N-1999;
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18-JUN-1999;
18-JUN-1999;
28-APR-1999;
30-APR-1999;
30-APR-1999;
04-MAY-1999;
06-MAY-1999;
06-MAY-1999;
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                                                                                                                                                                                                                                                                            SEAAKDLIYKWLERSPKKRISAHEALCHPWIVDEQAAPDKPLDPAVLSRLKQFSQMNKIK 313
                                                                                                                                                                                                                                                                                                                               193
                                                                                                                                                                       VAPEVIRKLYGPESDVWSAGVILYILLSGVPPFWAESEPGIFRQILLGKLDFHSEPWPSI 261
                                                                                                                                                                                                                                        KWALRVIAERLSEEFIGGLKELFKMIDTDNSGTITFEE----LKAGLKRVGSELMESEIK 369
                                                                                                                                                                                                                                                                                                                   EFGLCDTPLDDMIKEIDLDNDGKIDFSEFTAMMRKGD-GVGRSRTMMKNLNFNIADAFGV 488
                                                                             EIQIMHHLSEHPNVVRIKGTYEDSVFVHIVMEVCEGGELFDRIVSKGHFSERBAVKLIKT 133
                                                                                                  141
                                                                                                                               VAPEVLKKCYGPEIDVWSAGVILYILLSGVPPFWAETESGIFRQILQGKLDFKSDPWPTI 253
                                                                                                                                                                                                              KWALRVIAERLSEEEIGGLKELFKMIDTDNSGTITFDELKDGLKDGLKRVGSELMESEIK 381
                                         73
                                                           81
                        Gaps
                                       14 VLPYQTPRLRDHYLLGKKLGQGQFGTTYLCTEKSTSANYACKSIPKRKLVCREDYEDVWR
                                                    22 VLPQRIQNIREVYEVGRYLGQGQFGTIFECTRRASGGREACKSIPKRKLLCKEDYEDVWR
                                                                                          134 ILGVVEACHSLGVMHRDLKPENFLFDSPKDDAKLKATDFGLSVFYKPGQYLYDVVGSPYY
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    Length 512;
                     Indels
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   74.5%; Score 1932; DB 20;
ilarity 77.1%; Pred. No. 1.9e-163;
Conservative 51; Mismatches 51;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99US-0121825.
99US-0123180.
99US-0125788.
99US-0125788.
99US-012624.
99US-01276785.
99US-01276785.
99US-0128234.
99US-0128234.
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99US-0130510.
99US-0130891.
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             Similarity
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05-MAR-1999,
22-MAR-1999,
23-MAR-1999,
25-MAR-1999,
25-MAR-1999,
01-APR-1999,
06-APR-1999,
16-APR-1999,
16-APR-1999,
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    Query Match
Best Local Simi
Matches 370;
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PR 21-JUL-1999; 99US-0144814.

PR 22-JUL-1999; 99US-0146086.

PR 22-JUL-1999; 99US-0146086.

PR 22-JUL-1999; 99US-0146086.

PR 22-JUL-1999; 99US-0146089.

PR 22-JUL-1999; 99US-0145089.

PR 23-JUL-1999; 99US-0145192.

PR 23-JUL-1999; 99US-0145192.

PR 23-JUL-1999; 99US-0145218.

PR 24-JUL-1999; 99US-0145218.

PR 24-JUL-1999; 99US-0145218.

PR 25-JUL-1999; 99US-0145318.

PR 25-JUL-1999; 99US-0144318.

PR 25-JUL-1999; 99US-0144328.

PR 25-JUL-1999; 99US-015688.

PR 25-JUL-1999; 99U
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Protein identification, signal transduction pathway, metabolic pathway, hybridisation assay, genetic mapping, gene expression control, promoter, termination sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 DAKLKATDFGLSVFYKPGQYLYDVVGSPYYVAPEVLKKCYGPEIDVWSAGVILYILLSGV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          241 SGTITFEELKAGLKRVGSELMESEIKSLMDAADIDNSGTIDYGEFLAATLHINKMEREEN 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        301 LVVAFSYFDKDGSGYITIDELQQACTEFGLCDTPLDDMIKEIDLDNDGKIDFSEFTAMMK 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             284 IVDEQAAPDKPLDPAVLSRLKQFSQMNKIKKMALRVIAERLSEEFIGGLKELFKMIDTDN 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181 IVDEHAAPDKPLDPAVLSRLKQFSQMNKIKKMALRVIAERLSEEEIGGLKELFKMIDTDN 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     404 LVAAFSDFDKDGSGYITIDELQSACTEFGLCDTPLDDMIKEIDLDNDGKIDFSEFTAMMR 463
                                                                                                                                                                                                                                                                                                                                                                                                   104 MEVCEGGELFDRIVSKGHFSEREAVKLIKTILGVVEACHSLGVMHRDLKPENFLFDSPKD 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                              164 DAKLKATDFGLSVPYKPGQYLYDVVGSPYYVAPEVLKKCYGPEIDVWSAGVILYILLSGV 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            224 PPFWAETESGIFRQILQGKLDFKSDPWPTISEAAKDLIYKWLERSPKKRISAHEALCHPW 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SCTITFEELKAGLKRVGSELMESEIKSLMDAADIDNSCTIDYGEFLAATLHMNKMEREEI 403
                                                                                                                                                                                                                                                                                                                                                                    4; Gaps
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                                                                                                                                                                                                                                                                                                                                 Query Match 74.2%; Score 1924; DB 21; Length 399; Best Local Similarity 94.2%; Pred. No. 6.7e-163; Matches 373; Conservative 6; Mismatches 13; Indels 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Arabidopsis thaliana protein fragment SEQ ID NO: 37372.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   464 KGDGVGRSRTMMKNLNFNIADAFGVDG----EKSDD 495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      361 KGDGVGRSRTMRNNLNFNIAEAFGVEDTSSTAKSDD 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAG31158 standard; Protein; 483 AA
99US - 0159584

99US - 0160741

99US - 0160768

99US - 0160768

99US - 0160815

99US - 0160815

99US - 0160815

99US - 0160981

99US - 0161989

99US - 0161359

99US - 0161359
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18-OCT-1999;
21-OCT-1999;
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21-OCT-1999;
22-OCT-1999;
22-OCT-1999;
25-OCT-1999;
26-OCT-1999;
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AAG31158
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113-AUG-1999

120-AUG-1999

120-AUG-1999

120-AUG-1999

120-AUG-1999

120-AUG-1999

121-AUG-1999

121-AUG-1
990S-0121825
990S-0123180
990S-0123180
990S-0125788
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990S-0139463
990S-0140695
            25-FEB-2000; 2000EP-0301439
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990KS-0142803.
990KS-01442920.
990KS-01442920.
990KS-0144085.
990KS-01444085.
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990KS-014932.
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990KS-0149333.
990KS-0150864.
990KS-0150864.
990KS-0151333.

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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                                                                                   Arabidopsis thaliana protein fragment SEQ ID NO: 37371
                                                                  AAG31157 standard; Protein; 556 AA.
                                                                                                                                                                                                                                             99US-0121825.
99US-0123180.
99US-0125788.
99US-0125788.
99US-0126264.
99US-0127462.
99US-0127462.
99US-0129845.
99US-0129845.
99US-0120649.
99US-0130649.
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990S-0132486.
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99US-0134256.
99US-0134218.
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99US-0134221.
99US-0134370.
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99US-0134941,
99US-0135124,
99US-0135353
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99US-0137222
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99US-0138540
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                                                                                                     17-OCT-2000 (first entry)
                                                                                                                                                                           Arabidopsis thaliana
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06-MAY-1999;
06-MAY-1999;
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16-JUN-1999;
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       485 A 485
                                                                                     AAG31157;
                       483
                                               RESULT 8
AAG31157
ID AAG31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FSQMNKIKKMALRVIAERLSEERIGGLKELFKMIDTDNSGTITFEELKAGLKRVGSELME 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEIKSLMDAADIDNSGTIDYGEFLAATLHMNKMEREEILVAAFSDFDKDGSGYITIDELQ 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KSDPWPTISEAAKDLIYKWLERSPKKRISAHEALCHPWIVDEQAAPDKPLDPAVLSRLKQ 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                 EAVKLIKTILGVVEACHSLGVMHRDLKPENFLFDSPKDDAKLKATDFGLSVFYKPGQYLY 185
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              67.2%; Score 1742; DB 21; Length 483; 68.4%; Pred. No. 1.5e-146; ive 66; Mismatches 84; Indels 2
                                                                                     9903-0159294.
9903-0159295.
9903-0159329.
9903-0159330.
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99US-0159638.
99US-0159584.
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99US-0160767.
99US-0160768.
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99US-0161360.
99US-0161361.
99US-0161920.
99US-0161992.
99US-0155659.
99US-0156458.
99US-0156596.
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99US-0157865.
99US-0158029.
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99US-0158369.
99US-0159293.
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99US-0161406
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99US-0160815
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                           99US-0157117
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Best Local Similarity 68.49
Matches 329; Conservative
24-SEP-1999;
28-SEP-1999;
28-SEP-1999;
04-0CT-1999;
06-0CT-1999;
07-0CT-1999;
13-0CT-1999;
13-0CT-1999;
14-0CT-1999;
14-0CT-1999;
14-0CT-1999;
14-0CT-1999;
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14-0CT-1999;
15-0CT-1999;
16-0CT-1999;
17-0CT-1999;
18-0CT-1999;
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- 7 UW 1999 - 4 UW 1999 - 5 UW 1999 - 5 UW 1999 - 5 UW 1999 - 7 U	0.0 CUN-1999 0.0 C	22UL-1999; 22UL-1999; 23UL-1999; 23UL-1999; 23UL-1999; 24UL-1999; 27U
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14.04X 1999
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18.04X 1999
19.04X 1999
20.04X 1999
21.04X 1999
22.04X 1999
25.04X 1999
27.04X 1999
27.04X 1999
27.04X 1999
203.070 1999
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08-JUN-1999;
10-JUN-1999;
110-JUN-1999;
14-JUN-1999;
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    Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
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                                                                                                                  DVVGSPYYVAPEVLKKCYGPBIDVWSAGVILYILLSGVPPFWAETESGIFRQILQGKLDF 245
                                                                                                                                                                                              KSDPWPTISBAAKDLIYKMLERSPKKRISAHEALCHPWIVDEQAAPDKPLDPAVLSRLKQ 305
137 EDVEDVRREIQIMHHLAGHGSIVTIKGAYEDSLYVHIVMELCAGGELFDRIIQRGHYSER 196
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RR 03_AUG_1999 9US_0114932.

RR 03_AUG_1999 9US_0115204.

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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
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                                                                                                                                                                                                                                                   TDFGLSVFYKPGQYLYDVVGSPYYVAPEVLKKCYGPEIDVWSAGVILYILLSGVPPFWA-
                                                                                                                                                                                                                                                                                                     -----ETESGIFRQILQGKLDFKSDPWPTISEAAKDLIYKMLERSPKKRISAHE
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                                                                                                                                                          24;
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                                                                                                                                      65.7%; Score 1703; DB 21; Length 65.7%; Pred. No. 1e-142; ive 64; Mismatches 81; Indels
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65.7%; Pred. No. 1.1e-142;
iive 64; Mismatches 81;
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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
Arabidopsis thaliana protein fragment SEQ ID NO: 47640.
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                                                                               865 FVAMMOKGSIMG 876
                                                    458 FTAMMRKGDGVG 469
                                                                                                                                                                                                                                                                                                                                                      Arabidopsis thaliana
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29-MAR-1999;
01-APR-1999;
06-APR-1999;
08-APR-1999;
16-APR-1999;
21-APR-1999;
23-APR-1999;
23-APR-1999;
23-APR-1999;
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11-MAY-1999)

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14-NAY-1999)

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21-NAY-1999)

22-NAY-1999)
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30-APR-1999;
04-MAY-1999;
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New protein, useful for increasing tolerance to environmental stress, comprises a Protein Kinase Stress-Related Protein selected from
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                                                          169
                                                                                                                                                 748
                                                                                                                                                                                277
                                                                                                                                                                                                             808
                                                                                                                                                                                                                                                                                                                        628
                                                                                                                                                                                                                                         278 ALCHPWIVDEQAAPDKPLDPAVLSRLKQFSQMNKIKKMALRVIAERLSEBEIGGLKELFK 337
                                                                                                                                                                                                                                                                                                      MIDTDNSGTITFEELKAGLKRVGSELMESEIKSLMDAADIDNSGTIDYGEFLAATLHMNK 397
                                                                                                                                                                                                                                                                                                                                                                398 MEREBILVAAFSDFDKDGSGYITIDBLQSACTEFGLCDTPLDDMIKEIDLDNDGKIDFSE 457
                                                                                                                                                                                                  749 SEVNLFSMKYTETEQGIFEQVLHGDLDFSSDPWPSISESAKDLVRKMLVRDPKRRLTAHQ
                                                                                                                                                                                                                                                              809 VLCHPWVQIDGVAPDKPLDSAVLSRMKQFSAMNKFKKVALRVIAESLSEEEIAGLKQMFK
                                                                          689 IDFGLSMFFKRDDEVFTDVVGSPYYVAPEVLRKRYGPESDVWSAGVIVYILLSGVPPFWAG
                                                                                                                                                                                ------ETESGIFRQILQGKLDFKSDPWPTISEAKDLIYKMLERSPKKRISAHE
ANYACKSIPKRKLVCREDYEDVWREIQIMHHLSEHPNVVRIKGTYEDSVFVHIVMEVCEG
                GELFDRIVSKGHFSERBAVKLIKTILGVVEACHSLGVMHRDLKPENFLFDSPKDDAKLKA
                                                                                                                    TDFGLSVFYKPGQYLYDVVGSPYYVAPEVLKKCYGPEIDVWSAGVILYILLSGVPPFWA-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Physcomitrella patens CPK-2 protein, SEQ ID NO:39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAMS2842 standard; Protein; 549 AA.
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Sarria-Millan R;
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Sequences AAM52842 represent novel protein kinase stress-related proteins (PKSRPS) from the moss Physcomirella patens, and sequences ABA91081 represent full-length cDNAs encoding them. The CDNA sequences were obtained from expressed sequence tags (ESTS; ABA91056-ABA91056-ABA91068) derived from Physcomirella patens cDNA libraries The PKSRPs of the invention comprise protein kinase-6 (PK-6), protein kinase-8 (PK-7), protein kinase-8 (PK-8), protein kinase-17 (PK-7), protein kinase-8 (PK-8), protein kinase-17 (PK-7), protein kinase-18 (PK-8), protein kinase-18 (PK-7), mitogen-activated protein (MAP) kinase-18 (PK-5), casein kinase-18 (PK-7), mitogen-activated protein (MAP) kinase-18 (PK-7), MAP kinase-19 (PK-8), and calcium-dependent protein kinase-19 (PK-1), and calcium-dependent protein tinase-19 (PK-1), and calcium-dependent protein transgrauze-19 (PK-1), and calcium-dependent protein protein patents and sedds with increased to generate to confer transgenic plants and sedds with increased tolerance to salinity, drought cand are especially maize, wheat, rye, oat, triticale, rice, barley, cotton, rapesed, cassava, sunflower, tagetes, leguminous plants (e.g., sophean, peanut, Vicia species, alfalfa), solanaceous plants (e.g., sophean, peanut, vicia species, alfalfa), solanaceous plants (e.g., potato, tobacco, and are sayerian, peenmilal grasses and forage crops. The panner panner and as markers for specific regions of the panner panner.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RIKQFSQMNKIKKMALRVIAERLSEEEIGGLKELFKMIDTDNSGTITFEELKAGLKRVGS 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           riknfsaankokkulaikviaesiseeeivgiremfksidtonsgivifeelikegilkogs 428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ELMESEIKSLMDAADIDNSGTIDYGEFLAATLHMNKMEREEILVAAFSDFDKDGSGYITI 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      122 FSEREAVKLIKTILGVVEACHSLGVMHRDLKPENFLFDSPKDDAKLKATDFGLSVFYKPG 181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    69 PRPKPASKSVSGVLGKPLSDIRQSYILGRELGRGGFGVTYLCTDKMTNEAYACKSIAKRK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LVCREDYBDVWREIQIMHLSEHPNVVRIKGTYEDSVFVHIVMEVCEGGELFDRIVSKGH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5 PNPRRPSNT----VLPYQTPRLRDHYLLGKKLGQGQFGTTYLCTEKSTSANYACKSIPKRK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23; Length 549;
Protein kinases, Casein kinase homologs, MAP kinases or Calcium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       58.2%; Score 1509.5; DB 23; Lengt.
60.8%; Pred. No. 9.9e-126;
tive 70; Mismatches 112; Indels
                                                                      Claim 13; Fig 3M; 154pp; English
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Matches 290; Conservative
                        dependent protein kinases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   549 AA;
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AAG31159
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990S - 0139463

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23-AUG-1999;
23-AUG-1999;
 Protein identification, signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                             Arabidopsis thaliana protein fragment SEQ ID NO: 37373.
                                                                                                                                                                                       99US - 012182

99US - 0123180

99US - 0123786

99US - 0126785

99US - 0126785

99US - 0126785

99US - 0126785

99US - 012676

99US - 0132485

99US - 0132487

99US - 0132485

99US - 0132485

99US - 0132487

99US - 0134218

99US - 0134455

99US - 0139455

99US - 0139455
                                                                                                                                                                      25-FEB-2000; 2000EP-0301439
                            17-OCT-2000 (first entry)
                                                                                                           Arabidopsis thaliana.
                                                                                                                               EP1033405-A2.
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        AAG31159;
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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
          RVIAERLSEEBIGGLKELFKMIDTDNSGTITFEELKAGLKRVGSELMESEIKSLMDAADI 377
                                  DNSGTIDYGEFLAATLHMNKMEREEILVAAFSDFDKDGSGYITIDELQSACTEFGLCDTP 437
                                                                                                  LDDMIKEIDLDNDGKIDFSEFTAMMRKGD-GVGRSRTWMKNLNFNIADA 485
                                                                                                                                                                                                                                                                                                                                                                      Arabidopsis thaliana protein fragment SEQ ID NO: 58596.
                                                                                                                                                                                                                                                                   AAG46565 standard; Protein; 463 AA
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990S-0123180.
990S-0125788.
990S-0125784.
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99US-0135392.
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99US-0137222.
99US-0137528.
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23-APR-1999;
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28-APR-1999;
30-APR-1999;
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06-MAY-1999;
07-MAY-1999;
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14-MAY-1999;
14-MAY-1999;
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18-MAY-1999;
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05-MAY-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 VEACHSLGVVHRDLKPENFLLVNKDDDFSLKAIDFGLSVFFKFGQIFTDVVGSPYYVAPE 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   78 MHHLSEHPNVVRIKGTYEDSVFVHIVMEVCEGGELFDRIVSKGHFSEREAVKLIKTILGV 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     138 VEACHSLGVMHRDLKPENFLFDSPKDDAKLKATDFGLSVFYKPGQYLYDVVGSPYYVAPE 197
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69.4%; Pred. No. 7.1e-126;
ive 56; Mismatches 67;
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990S-0161405
990S-0161359
990S-0161350
990S-0161360
990S-0161360
990S-0161923
990S-0161992
990S-0161992
99US-0150566.
99US-0150884.
99US-0151066.
99US-0151080.
99US-0151080.
99US-0151033.
99US-0151438.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
25-AUG-1999;
26-AUG-1999;
27-AUG-1999;
27-AUG-1999;
31-AUG-1999;
31-AUG-1999;
31-AUG-1999;
31-AUG-1999;
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32-AUG-1999;
33-AUG-1999;
34-AUG-1999;
35-AUG-1999;
36-AUG-1999;
36-AUG-1999;
36-AUG-1999;
36-AUG-1999;
36-AUG-1999;
37-AUG-1999;
38-AUG-1999;
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99US - 0147103 99US - 0147416 99US - 0147413 99US - 0147413 99US - 0147413 99US - 0147413 99US - 0147413 99US - 0148171 99US - 0148171 99US - 0148171 99US - 0148171 99US - 0149172 99US - 0149172 99US - 0149173 99US - 0149173 99US - 0149173 99US - 0149173 99US - 015173 99US - 015174 99US - 015174	
06-Aug-1999999999999999999999999999999999999	
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Score 1501; DB 21; Length 463; Pred. No. 4.4e-125;

57.9%; 61.4%;

Query Match Best Local Similarity comprises: (1) introducing into 1 or more plant protoplasts:

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                                                                                  187
                                                                                                                                                              EIDVWSAGVILYILLSGVPPFWAETESGIFRQILQGKLDFKSDPWPTISEAAKDLIYKML 265
                                                                                                                                                                             325
                                                                                                                                                                                                                         248 NSDFKQRLTAAQVLNHPWIKEDGEAPDVPLDNAVMSRLKQFKAMNNFKKVALRVIAGCLS 307
                                                                                                                                                                                                                                                         EEEIGGLKELFKMIDTDNSGTITFEELKAGLKRVGSELMESEIKSLMDAADĮDNSGTIDY 385
                                                                                                                                                                                                                                                                       GEFLAATLHMNKMEREEILVAAFSDFDKDGSGYITIDELQSACTEFGLCD-TPLDDMIKE 444
                                                                                                                                                                                                                                                                                                                    GEFIAATWHINRLDREEHLYSAFQHFDKDNSGYITMEELEQALREFGWNDGRDIKEIISE 427
                                                                    NVVRIKGTYEDSVFVHIVMEVCEGGELFDRIVSKGHFSEREAVKLIKTILGVVEACHSLG 145
                                                                                                                 VMHRDLKPENFLFDSPKDDAKLKATDFGLSVFYKPGQYLYDVVGSPYYVAPEVLKKCYGP 205
 Gaps
                                            67
                       YLLGXKLGQGQFGTTYLCTEKSTSANYACKSIPKRKLVCREDYEDVWREIQIMHLSEHP 85
                                     ERSPKKRISAHEALCHPWIVDEQAAPDKPLDPAVLSRLKQFSQMNKIKKMALRVIAERLS
 .
9
 Indels
92;
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79; Mismatches
 Conservative
 Matches 281;
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AAG65758 standard; Protein; 280 AA. 07-JAN-2002 (first entry) AAG65758 RESULT 15 AAG65758

ATCDPK2 kinase domain sequence.

Plant protoplast, gene expression, Arabidopsis, PK, CDPK, ATCDPK2, calcium activated protein kinase, calcium dependant protein kinase

Arabidopsis thaliana

WO200168920-A1

20-SEP-2001

13-MAR-2001; 2001WO-US07999

13-MAR-2000; 2000US-189074P.

GEHO) GEN HOSPITAL CORP

Sheen J;

WPI; 2001-611395/70.

Using plant protoplast expression systems for rapidly screening libraries of nucleic acids to identify gene that modulate expression of target genes -

Examples; Fig 3B; 95pp; English.

The invention provides a high through-put assay for rapidly screening a library of nucleic acid molecules to identify a gene product that modulates expression of a gene of interest in plant protoplasts. The

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(a) reporter gene construct operably linked to a promoter of a gene of interest, and (b) a member of a library of nucleic acid molecules (the library control of the molecules (the library member is expressed in the plant protoplasts), and (2) screening the protoplasts to determine whether the amount of gene expression of the preparter gene construct changes in response to the expression of the library members, a change in gene expression of the reporter gene construct identifying the gene product expressed by the library member as in that modulates expression of the gene of interest. The present sequence protocell kinase (CDPK) ATCDPRZ kinase domain.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 LIKTILGVVEACHSLGVMHRDLKPENFLFDSPKDDAKLKATDFGLSVFYKPGQYLYDVVG 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DVWREIQIMHHLSEHPNVVRIKGTYEDSVFVHIVMEVCEGGELFDRIVSKGHFSERAVK
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                                                                                                                                                                                                                                                                                  57.8%; Score 1500; DB 22; Length 280; 100.0%; Pred. No. 2.6e-125; ive 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        241 WPTISEAAKDLIYKMLERSPKKRISAHEALCHPWIVDEQA 280
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                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.
Matches 280; Conservative
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                                                                                                                                                                                                                                                     Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: FICENOME READABLE FORM:
MEDIUM TYPE: FICENOME READABLE FORM:
MEDIUM TYPE: FICENOME RECOMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPATE: FACENOME RECOMES SOFTWARE: PATENTIN Release #1.0, Version #1.30B
CURRENT APPLICATION NUMBER: US/07/951,715A
FILING DATE: 25-SEP-1992
CLASSIFICATION 800
PRIOR APPLICATION 907A:
APPLICATION WUMBER: US 07/772,027
ATRONEY/AGENT INFORMATION:
MANNE: COMMATION:
MANNE: ACCOUNTING MANNESS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Spriil, W. Murray
REGISTRATION NUMBER: 32,943
REFERENCE/DOCKET NUMBER: S-18805/A/CGC 1577/CIP
TELECOMMUNCATION INFORMATION:
TELEPHONE: (919)541-8615
TELEFRONE: (919)541-8689
US-09-272-796-19
US-09-457-040B-31
US-09-257-240B-31
US-07-857-224B-19
US-09-800-960-2
US-09-800-960-2
US-09-800-960-2
US-08-715-568A-1
US-08-715-568A-1
US-08-715-568A-1
US-08-919-627-3
US-09-096-245-3
US-09-457-040B-30
                                                                                                                                            US-08-678-989-5
US-09-272-796-5
US-08-459-448A-23
US-08-459-595A-23
US-08-459-595A-23
                                                                                                                                                                                                                                             ALIGNMENTS
                                                                                                                                                                                                                                                                                                                        APPLICANT: Koziel, Michael G.
APPLICANT: Desai, Nallni M.
APPLICANT: Desai, Nallni M.
APPLICANT: Ramer, Vance C.
APPLICANT: Warren, Gregory W.
APPLICANT: Evola Stephen V.
APPLICANT: Wright, Martha S.
APPLICANT: Wright, Martha S.
APPLICANT: Merlin, Ellis J.
APPLICANT: Merlin, Ellis J.
APPLICANT: Denman, Cludy G.
APPLICANT: Bowman, Cludy G.
APPLICANT: Bowman, Cludy G.
APPLICANT: Bowman, Cludy G.
APPLICANT: Bowman, Cludy G.
APPLICANT: Suttie, John L.
ITLE OF INVENTION: INSECTICIDAL ACTIV.
NUMBER OF SEQUENCES: 94
CORRESPONDENCE ADDRESS:
ADDRESSE: CIRA-GEIGY CORPORATION: SYNTHETIC DNA SEQUENCES: STREET: New V.--
                                                                                                                                                                                                                                                                                                      ; Sequence 25, Application US/07951715A; Patent No. 5625136; GENERAL INFORMATION:
               STATE: New York
COUNTRY: USA
   RESULT 1
US-07-951-715A-25
                          (without alignments)
662.016 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 25,
Sequence 25,
Sequence 0, 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 18,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 25,
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Sequence 17,
Sequence 22,
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                                                                                                                                     US-09-848-806-1
2593
1 METKPPRRPSNTVLPYQTP......KNLNFNIADAFGVDGEKSDD
                                                                                       February 13, 2003, 21:08:08; Search time 22 Seconds
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/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
                GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-07-951-715A-25
US-08-455-448A-25
US-08-459-504B-25
US-08-459-444-25
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US-08-459-464-25
US-08-459-464-22
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US-08-459-464-22
US-08-459-444-21
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US-08-459-444-21
US-08-459-464-21
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US-08-459-464-21
US-08-459-464-21
US-08-464-164-2
US-08-347-801-19
US-08-464-164-2
US-08-347-801-19
US-08-464-164-2
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US-08-348-06-2
US-08-348-06-2
US-08-464-164-2
US-08-348-06-2
US-08-257-801-19
US-08-464-164-2
US-08-348-06-2
US-08-257-801-19
                                                                                                                                                                                                                                                Total number of hits satisfying chosen parameters:
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                                                                                                                                                                                                                                                                                                        Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                - protein search, using sw model
                                                                                                                                                                                     BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                         Issued Patents AA:*
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Maximum DB seq length: 200000000
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Perfect score:
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                                                                                                                                                                                      Scoring table:
                                                                 OM protein
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REPERBNCE/DOCKST NUMBER: CGC 1577/CIP/DIV4
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8582
                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 463 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                 New York
                                                                                                                                                                                    10591-9005
                                                                                                                                                                    USA
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                                                                                                                                                                 COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           134 ILGVVEACHSLGVMHRDLKPENFLFDSPKDDAKLKATDFGLSVFYKFGQYLYDVVGSFYY 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                194 VAPEVLKKCYGPEIDVWSAGVILYILLSGVPPFWAETESGIFRQILQGKLDFKSDPWPTI 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        254 SEAAKDLIYKMLERSPKKRISAHEALCHPWIVDEQAAPDKPLDPAVLSRLKQFSQMNKIK 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             314 KMALRVIAERLSEEFIGGLKELFKMIDTDNSGTITFEELKAGLKRVGSELMESEIKSLMD 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      374 AADIDNSCTIDYGEFLAATLHMNKWEREEILVAAFSDFDKDGSGYITIDELQSACTEFGL 433
                                                                                                                                                                                                                                                                                                              2; Gaps
                                                                                                                                                                                                                                                                                                                                                                     1 VLPQRTQNIREVYEVGRKLGQGQFGTTFECTRRASGGKFACKSIPKRKLLCKEDYEDVWR 60
                                                                                                                                                                                                                                                                                                                                                 14 VLPYQTPRLRDHYLLGKKLGQQQPGTTYLCTEKSTSANYACKSIPKRKLVCREDYEDVWR 73
                                                                                                                                                                                                                                                                     Query Match 74.3%; Score 1927; DB 1; Length 463; Best Local Similarity 78.7%; Pred. No. 1e-152; Matches 365; Conservative 49; Mismatches 48; Indels 7
                                                                                                                                                                              LOCATION: 1..463
COTER INFORMATION: /note= "protein sequence for OTHER INFORMATION: soybean CDFK as shown in Figure 34."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          434 CDIPLDDMIKEIDLDNDGKIDFSEFTAMMRKGD-GVGRSRIMMK 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                421 DDIHIDDMIKEIDQDNDGQIDYGEFAAMMRKGNGGIGR-RTMRK 463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 25, Application US/08459448A; Patent No. 5859336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rothstein, Steven J.
Bowman, Cindy G.
Dawson, John L.
Dunder, Erik M.
Pace, Gary M.
Suttie, Janet L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Koziel, Michael G.
Desai, Nalini M.
Lewis, Kelly S.
Kramer, Vance C.
Wartren, Gregory W.
Evola, Stephen V.
Crossland, Lyle D.
Wright, Martha S.
Merlin, Ellis B.
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 463 amino acids
                                   LENGTH: 463 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                          MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                 NAME/KEY: Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Koziel,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 2
US-08-459-448A-25
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APPLICANT:
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61 BIQIMEHLSEHANVVRIEGTYEDSTAVHLVMELCEGGELFDRIVQKGHYSERQAARIKT 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181 VAPEVLRKLYGPESDVWSAGVILYILLSGVPPFWAESEPGIFRQILLGKLDFHSEPWPSI 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  134 ILGVVEACHSLGVVHRDLKPENFLFDSPKDDAKLKATDFGLSVFYKPGQYLYDVVGSPYY 193
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74.3%; Score 1927; DB 2; Length 463;
Best Local Similarity 78.7%; Pred. No. 1e-152;
Matches 365; Conservative 49; Mismatches 48; Indels 2
TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE CORRESPONDENCE 94

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: Protein
LOCATION: 1..463
OTHER INFORMATION: /note= "protein sequence for
OTHER INFORMATION: soybean CDPK as shown in Figure 34."
                                                                                                                                   ADDRESSEE: No. 5859336artis Corporation
STREET: Patent & Trademark Dept., 520 White Plains
STREET: Rd., POB 2005
CITY: Tarrytown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM: PC_DOS/MD-LOG
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,448A
FILING DATE: 0.2-UN-1995
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/951,715
FILING DATE: 0.4-0.777,027
FILING DATE: 0.4-0.777,027
FILING DATE: 0.4-0.771,027
FILING DATE: 0.4-0.77191
ATTORNEY AGENT INFORMATION:
NAME: Pace, Gary M.
REGISTRATION NUMBER: 4 0403
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HYPOTHETICAL: NO
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APPLICANT:
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   301 KWALRVIARRLSEBEIGGLKELFKMIDTDNSGTITFDELKDGLKRVGSELMESEIKDLMD 360
                                                                                            374 AADIDNSGTIDYGEFLAATLHMNKMEREEILVAAFSDFDKDGSGYITIDELQSACTEFGL 433
                                                                                                                                   APPLICANT: ROCKERTO, CINGY G.
APPLICANT: Boownen, Cindy G.
APPLICANT: Boownen, Cindy G.
APPLICANT: Dawson, John L.
APPLICANT: Dawson, John L.
APPLICANT: Dawson, John L.
APPLICANT: Bace, Gary M.
APPLICANT: Suttie, Janet L.
TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE NUMBER OF SEQUENCES: 94
CORRESPONDENCE ADDRESS:
ADDRESSE: No. 6018104artis Corporation STREET: Patent & Trademark Dept., 520 White Plains CITY: Tarrytown STREET: Patent & Trademark Dept., 520 White Plains Dept., 520 White Dept., 520 
                                                                                                                                                                                                                  434 CDTPLDDMIKEIDLDNDGKIDFSEFTAMMRKGD-GVGRSRTMMK 476
                                                                                                                                                                                                                                                      CGC 1577/CIP/DIV3
                                                                                                                                                                                                                                                                                                                                                                                                                  December 25, Application US/0845959A Patent No. 6018104 GENERAL INFORMATION: APPLICANT: Koziel, Michael G. APPLICANT: Ceviel, Michael G. APPLICANT: Lewis, Kally S. APPLICANT: Besi, Nalini M. APPLICANT: Warren, Gregory W. APPLICANT: Warren, Gregory W. APPLICANT: Wright, Martha S. APPLICANT: Wright, Martha S. APPLICANT: Wright, Martha S. APPLICANT: Weight, Martha S. APPLICANT: Rethatein, Steven J. APPLICANT: Bowmen, Clindy G. APPLICANT: Bowmen, Clindy G. APPLICANT: Bowmen, Clindy G. APPLICANT: Dunder, Brik M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acia
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             314 KWALRVIAERLSEEEIGGLKELFKWIDTDNSCTITFEELKAGLKRVGSELMESEIKSLMD 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           374 AADIDNSGTIDYGEFLAATLHMNKMEREEILVAAFSDFDKDGSGYITIDELQSACTEFGL 433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 BIQIMEHLSEHANVVRIBGTYBBSTAVHLVWELCEGGELFDRIVQKGHYSERQARLIKT 120
                                                                                                                                                                                                                                                                                                                                                                                                            134 ILGVVEACHSLGVMHRDLKPENPLFDSPKDDAKLKATDFGLSVFYKPGQYLYDVVGSPYY 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          253
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                                                                                                                                                                               Gaps
                                                                                                                                                                                                                       14 VLPYQTPRLRDHYLLGKKLGQGQFGTTYLCTEKSTSANYACKSIPKRKLVCREDYEDVWR 73
                                                                                                                                                                                                                                                       194 VAPEVLKKCYGPEIDVWSAGVILYILLSGVPPFWAETESGIFRQILQGKLDFKSDPWPTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5;
                                                                                                                           Query Match 74.3%; Score 1927; DB 3; Length 463; Best Local Similarity 78.7%; Pred. No. 1e-152; Matches 365; Conservative 49; Mismatches 48; Indels
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                                          /note= "protein sequence for soybean CDPK as shown in Figure 34."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  434 CDTPLDDMIKEIDLDNDGKIDFSBFTAMMRKGD-GVGRSRTMMK 476
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STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 25, Application US/08459504B, Patent No. 6075185, GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Desai, Nalini M.
Lewis, Kelly S.
Kramer, Vance C.
Warren, Gregory W.
Evola, Stephen V.
Crosland, Lyle D.
Wright, Martha S.
Merlin, Blis J.
Launis, Karen J.
Rothstein, Steven J.
Rothstein, Steven J.
Bowson, John L.
Dunder, Erik M.
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NAME/KEY: Protein
LOCATION: 1..463
OTHER INFORMATION: 9
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CORRESPONDENCE ADDRESS:
ADDRESSEE: NO. 6121014artis Agribusiness Biotechnology Research, Inc. STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: /note= "protein sequence for soybean CDPK as shown in Figure 34."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Launis, Karen L.
TITLE OF INVENTION: METHOD FOR PRODUCING A PLANT-OPTIMIZED NICLEL ACID CODING SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Meigs, J. Timothy REGISTRATION NUMBER: 38,241 REFERENCE DOCKET NUMBER: S-18805/P1/CGC1577/CIP/DIV6 TELECOMMUNICATION: INFORMATION:
434 CDTPLDDMIKEIDLDNDGKIDFSEFTAMMRKGD-GVGRSRTMMK 476
                                    421 DDIHIDDMIKEIDQDNDGQIDYGEFAAMMRKGNGGIGR-RIMRK 463
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74.3%; Score 1927; DB 3;
Best Local Similarity 78.7%; Pred. No. 1e-152;
Matches 365; Conservative 49; Mismatches 48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Vers
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,444A
FILING DATE: 02-Jun-1995
CLASSIFICATION: <UNknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/951,715
FILING DATE: 25-SEP-1992
APPLICATION NUMBER: US 07/772,027
FILING DATE: 04-OCT-1991
ATTORNEY/AGENT INFORMATION:
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SEQUENCE DESCRIPTION: SEQ ID NO: 25:
                                                                                                                                                                                                           Sequence 0, Application US/08459444A Patent No. 6121014 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (919)541-8587
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                                                                                                                                                                                                                                                                                                                                        Desai, Nalini M.
Lewis, Kelly S.
Kramer, Vance C.
Warren, Gregory W.
Evola, Stephen V.
Crossland, Lyle D.
Wright, Martha S.
Merlin, Ellis J.
                                                                                                                                                                                                                                                                                                                 APPLICANT: Koziel, Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear MOLECULE TYPE: protein HYPOTHETICAL: NO FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
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US-08-459-444-25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   301 KWALKVIAERLSEEFIGGLKELFKMIDTDNSGTITFDELKDGLKRVGSELMESEIKDLMD 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     74 BIQIMHHLSEHPNVVRIKGTYEDSVFVHIVMEVCEGGELFDRIVSKGHFSEREAVKLIKT 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14 VLPYQTPRLRDHYLLGKKLGQGQFGTTYLCTEKSTSANYACKSIPKRKLVCREDYEDVWR 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               74.3%; Score 1927; DB 3; Length 463; 78.7%; Pred. No. 1e-152;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "protein sequence for soybean CDPK as shown in Figure 34."
                                                                                                                                                                                                 Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                       FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/459,595
FILING DATE: 02-0707195
APPLICATION NUMBER: US 07/951,715
FILING DATE: 25-SEP-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/772,027
FILING DATE: 04-0CT-1991
ATTORNEY AGENT INFORMATION:
NAME: Weigs, J. Timothy
REGISTRATION NUMBER: 38,241
REGISTRATION NUMBER: 38,241
REGISTRATION NUMBER: 38,241
REGISTRATION NUMBER: GGC1577/CIP/DIV
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 1000 DATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 49; Mismatches
                                                                                                                                                                                                                                                                US/08/459,504B
                                                                                                                                         COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (919) 541-8689
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 463 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 78.74
Matches 365; Conservative
                                                                                                                                                                                                     SOFTWARE: Patentin Rel
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
                   COUNTRY: USA
ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
NAME/KEY: Protein
LOCATION: 1..463
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-459-504B-25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEAAKDLIYKWLERSPKKRISAHEALCHPWIYDEQAAPDKPLDPAVLSRLKQFSQMNKIK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 IVEVVBACHSLGVMHRDLKPENFLFDTIDEDAKLKATDFGLSVFYKPGESFCDVVGSPYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    194 VAPEVLKKCYGPEIDVWSAGVILYILLSGVPPFWAETESGIFRQILQGKLDFKSDPWPTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14 VLPYQTPRLRDHYLLGKKLGQGQFGTTYLCTEKSTSANYACKSIPKRKLVCREDYEDVWR
                                          REFERENCE/DOCKET NUMBER: S-18805H
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8587
TELEFAX: (919)541-8687
INFORMATION FOR SEQ ID NO: /note= "protein sequence for soybean CDPK as shown in Figure 34."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      74.3%; Score 1927; DB 4; Length 463; 78.7%; Pred. No. 1e-152; ive 49; Mismatches 48; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                434 CDTPLDDMIKEIDLDNDGKIDFSEFTAMMRKGD-GVGRSRTMMK 476
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Patent No. 6262345
GENERAL INFORMATION:
APPLICANT: Allen, Steve
APPLICANT: Lee, Jian Ming
TITLE OF INVENTION: Plant Protein Kinases
FILE REFERENCE: BB-1171
CURRENT APPLICATION NUMBER: US/09/347,801
CURRENT FILING DATE: 1999-07-02
EARLIER APPLICATION NUMBER: 60/092,438
EARLIER PILING DATE: July 10, 1998
NUMBER OF SEQ ID NOS: 23
SOFTWARE: MICROSOft Office 97
                                                                                                                                                                                                                                                                                                                                                                                               LOCATION: 1..463
SEQUENCE DESCRIPTION: SEQ ID NO: 25:
NAME: Meigs, J. Timothy REGISTRATION NUMBER: 38,241
                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 463 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                    STRANDEDNESS: Single TOPOLOGY: linear MOLECULE TYPE: protein PYPOTHETICAL: NO FEATURE:
                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 78.7%
Matches 365; Conservative
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US-09-347-801-17
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CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6320100artis Agribusiness Biotechnology Research, Inc.
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: NC
                                                                                                                                                                         253
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      301 KWALRVIAERLSEEEIGGLKELFKMIDTDNSGTITFDELKDGLKRVGSELMESEIKDLMD 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       433
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                                                                                                                                           193
                                                                                                                                                                                                                                                                                                                                 SEAAKDLIYKWLERSPKKRISAHEALCHPWIVDEQAAPDKPLDPAVLSRLKQFSQMNKIK
                                                                             194 VAPEVLKKCYGPEIDVWSAGVILYILLSGVPPFWAETESGIFRQILQGKLDFKSDPWPTI
                                                                                                                                                                                                                                                                                                                                                                                                                             KMALRVIAERLSEBEIGGLKELFKMIDTDNSGTITFEBLKAGLKRVGSELMESEIKSLMD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AADIDNSGTIDYGEFLAATLHMNKMEREEILVAAFSDFDKDGSGYITIDELQSACTEFGL
    1 VLPQRIQNIREVYEVGRKLGQGQFGTTFECTRRASGGKFACKSIPKRKLLCKEDYEDVWR
                                                    EIQIMHHLSEHPNVVRIKGTYEDSVFVHIVMEVCEGGELFDRIVSKGHFSEREAVKLIKŢ
                                                                                                                                           ILGVVEACHSLGVMHRDLKPENFLFDSPKDDAKLKATDFGLSVFYKPGQYLYDVVGSPYY
                                                                                                                                                                                                                                                                               181 VAPEVLRKLYGPESDVWSAGVILYILLSGVPPFWAESEPGIFRQILLGKLDFHSEPWPSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED INSECTICIDAL ACTIVITY IN MAIZE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: FLORDY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
RAPLICATION NUMBER: US/09/547,422
FILING DATE: 11-Apr-2000
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   434 CDTPLDDMIKEIDLDNDGKIDFSEFTAMMRKGD-GVGRSRTMMK 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DDIHIDDMIKEIDQDNDGQIDYGEFAAMMRKGNGGIGR-RIMRK 463
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APPLICATION NUMBER: US 08/459,595
FILING DATE: 02-0UN-1995
APPLICATION NUMBER: US 07/951,715
FILING DATE: 25-SEP-1992
APPLICATION NUMBER: US 07/772,027
FILING DATE: 04-0CT-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 0, Application US/09547422

Patent No. 6320100
GENERAL INFORMATION:
PAPLICANT: Koziel, Michael G.
Kramer, Vance C.
Warren, Gregory W.
Evola, Stephen V.
Crossland, Lyle D.
Wright, Martha S.
Wartha S.
Martha S.
Martha S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA
ZIP: 27709
COMPUTER READABLE FORM:
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RESULT 9
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                                                                                                                                                                                                                                                                                                                                         113 FDRIVSKGHFSEREAVKLIKTILGVVEACHSLGVMHRDLKPENFLFDSPKDDAKLKATDF 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 233 GIFROILOGKLDFKSDPWPTISEAAKDLIYKMLERSPKKRISAHEALCHPWIVDEQAAPD 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    353 KAGLKRVGSELMESEIKSLMDAADIDNSGTIDYGEFLAATLHMNKWEREEILVAAFSDFD 412
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     173 GLSVFYKPGQYLYDVVGSPYYVAPEVLKKCYGPEIDVWSAGVILYILLSGVPPFWAETES 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                293 KPLDPAVLSRLKOFSOMNKIKKMALRVIAERLSEEEIGGLKELFKMIDTDNSGTITFEEL 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        413 KDGSGYITIDELQSACTEFGLCDTPLDDMIKEIDLDNDGKIDFSEFTAMMRKGDGVGRSR 472
                                                                                                                                  Query Match
64.5%; Score 1672.5; DB 4; Length 639;
Best Local Similarity 66.2%; Pred. No. 2.6e-131;
Matches 318; Conservative 66; Mismatches 83; Indels 13; Gaps
                                                                                                                                                                                                                       5 PNPR-RPS-----NTVLPYQTPRLRDHYLLGKKLGQGQFGTTYLCTEKSTSANY 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Desai, Mainael G.
APPLICANT: Lewis, Kelly S.
APPLICANT: Lewis, Kelly S.
APPLICANT: Warren, Gregory W.
APPLICANT: Bovla, Stephen V.
APPLICANT: Evola, Stephen V.
APPLICANT: Wright, Martha S.
APPLICANT: Wright, Martha S.
APPLICANT: Martin, Ellis J.
APPLICANT: Martin, Ellis J.
APPLICANT: Rothstein, Steven J.
APPLICANT: Bowman, Cindy G.
APPLICANT: Bowman, Cindy G.
APPLICANT: Bowman, Cindy G.
APPLICANT: Bowman, Cindy G.
APPLICANT: Bowco, John L.
APPLICANT: Bowco, John L.
APPLICANT: Suttis, Janet L.
TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE S.
ADDRESSEE: CIBA-GEIGY COTTON SKREY ADDRESS:
ADDRESSEE: CIBA-GEIGY COTTON SKREY CITY: T SKV1'*-
                                                                                                                                  Query Match
Best Local Similarity
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STATE: New York
COUNTRY: USA
                                          TYPE: PRT
; ORGANISM: Zea mays
US-09-347-801-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-07-951-715A-22
SEQ ID NO 17
LENGTH: 639
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). LOCATION: 1..464
) OTHER INFORMATION: /note= "derived protein sequence of ; OTHER INFORMATION: pollen specific CDPK as disclosed in Figure 34."
US-07-951-715A-22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            82 SEHPNVVRIKGTYEDSVFVHIVMEVCEGGELFDRIVSKGHFSEREAVKLIKTILGVVEAC 141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    262 YXWLERSPKKRISAHEALCHPWIVDEQAAPDKPLDPAVLSRLKQFSQMNKIKKWALRVIA 321
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      309 GCLSEERITGLKEMFKNIDKDNSGTITLDELKHGLAKHGPKLSDSEMEKLMEAADADGNG 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        382 TIDYGEFLAATLHWNKMEREEILVAAFSDFDKDGSGYITIDELQSACTEFGLCDT-PLDD 440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       369 LIDYDEFVTATVHMYKLDREEHLYTAFQYFDKDNSGYITKEELBHALKEQGLYDADKIKD 428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 55.4%; Score 1437.5; DB 1; Length 464; Best Local Similarity 60.9%; Pred. No. 6.7e-112; Matches 271; Conservative 70; Mismatches 103; Indels 1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9 VRATYSMGKELGRGQFGVTHLCTHRTSGEKLACKTIAKRKLAAREDVDDVRREVQIMHHL 68
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COMPUTER EAGABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Eloppy disk
COMPUTER: Eloppy disk
COMPUTER: Elm PC Compatible
COMPUTER: Elm PC Compatible
COMPUTER: Patentin Release #1.0, Version #1.30B
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/951,715A
FILING DATE: 25-SEP-1992
CLASSIFICATION: 80 07/772,027
FILING DATE: 04-0CT-1991
APPLICATION NUMBER: US 07/772,027
FILING DATE: 04-0CT-1991
ATTORNEY/AGRATION: MAITAN
NAME: SPELILI, W. MAITAN
REPERBACE/OCCKET NUMBER: 32-943
REPERBACE/OCCKET NUMBER: S-18805/A/CGC 1577/CIP
TELECOMMUNICATION INFORMATION:
TELECHMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
TOWNSTICE CHARACTERISTICS:
TOWNSTICE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         441 MIKEIDLDNDGKIDFSEFTAMMRKG 465
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
STRANDEDNESS: si
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RESULT 10
US-08-459-595A-22
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60.9%; Pred. No. 6.7e-112;
live 70; Mismatches 103; Indels 1; Gaps;
                                                                                                                                                                                                                                                   APPLICANT: Rothsein, Steven J.
APPLICANT: Rothsein, Cindy G.
APPLICANT: Bowman, Cindy G.
APPLICANT: Dawson, John L.
APPLICANT: Dunder, Erik M.
APPLICANT: Pace, Gary M.
APPLICANT: Sutie, Janet L.
TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED NUMBER OF SEQUENCES: 94
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: No. 5859336artis Corporation STREET: Patent & Trademark Dept., 520 White Plains STREET: Rd., POB 2005
CITY: Tarrytown
CITY: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CUDNIKT: 10905

CUNTRY: 10591-9005

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC COMPATIBLE
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,448A
FILING DATE: 02-UN-1995
CLASSIFICATION NUMBER: US 07/951,715
FILING DATE: 25-SEP-1992
PRIOR APPLICATION NUMBER: US 07/772,027
PTILING DATE: 04-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Pace, Gary M.
REGISTRATION NUMBER: 40403
REFERENCE/POCKET NUMBER: CGC 1577/CIP/DIV4
TELECOMMUTICATION INFORMATION:
TELEPHONE: (919)541-8582
             Sequence 22, Application US/08459448A Patent No. 5859336 GENERAL INFORMATION:
                                                                 Moziel, Michael G.
Desai, Nalini M.
Lewis, Kelly G.
Kramer, Vance C.
Warren, Gregory W.
Evola, Stephen V.
Crossland, Lyle D.
Wright, Martha S.
Merlin, Ellis J.
Launis, Karen L.
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 464 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 60.99
Matches 271; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS: single
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US-08-459-448A-22
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Best Local
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LRDHYLLGKKLGQGQFGTTYLCTEKSTSANYACKSIPKRKLVCREDYEDVWREIQIMHHL 81

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369 LIDYDEFVTATVHANKLDREEHLYTAFQYFDKDNSGYITKEELEHALKEQGLYDADKIKD 428
                                                                                                                                    69 SGQPNVVGLRGAXEDKQSVHLVMELCAGGELFDRIIARGQYTERGAAELLRAIVQIVHTC 128
                                                                                                                                                                                                                  142 HSLGVMHRDLKPENFLFDSPKDDAKLKATDFGLSVFYKPGQYLYDVVGSPYYVAPEVLKK 201
                                                                                                                                                                                                                                                     261
                                                                                                                                                                                                                                                                                                                                                                                                                                                              262 YKMLERSPKKRISAHEALCHPWIVDEQAAPDKPLDPAVLSRLKOFSOMNKIKKMALRVIA 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        249 KKMLNINPKERLTAFQVLNHPWIKEDGDAPDTPLDNVVLDRLKQFRAMNQFKKAALRIIA 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            309 GCLSEEEITGLKEMFKNIDKDNSCTITLDELKHGLAKHGPKLSDSBMEKLMEAADADGNG 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             382 TIDYGEFLAATLHMNKMEREEILVAAFSDFDKDGSGYITIDELQSACTEFGLCDT-PLDD 440
                                                                                                 SEHPNYVRIKGTYEDSVFVHIVMEVCEGGELFDRIVSKGHFSEREAVKLIKTILGVVEAC 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      322 ERLSEEBIGGLKELFKMIDTDNSGTITFEBLKAGLKRVGSELMESBIKSLMDAADIDNSG 381
9 VRATYSMGKELGRGQPGVTHLCTHRTSGEKLACKTIAKRKLAAREDVDDVRREVQIMHHL 68
                                                                                                                                                                                                                                                                                                                                             202 CYGPEIDVWSAGVILYILLSGVPPFWAETESGIFRQILQGKLDFKSDPWPTISBAAKDLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Roziel, Maini M.
APPLICANT: Desai, Nalini M.
APPLICANT: Desai, Nalini M.
APPLICANT: Eweis, Kelly S.
APPLICANT: Kramer, Vance C.
APPLICANT: Warren, Gregory W.
APPLICANT: Wright, Martha S.
APPLICANT: Wright, Martha S.
APPLICANT: Wright, Martha S.
APPLICANT: Wright, Martha S.
APPLICANT: Worlin, Ellis J.
APPLICANT: Bowman, Cludy G.
APPLICANT: Bowman, Cludy G.
APPLICANT: Dawson, John L.
APPLICANT: Basco, Gary M.
APPLICANT: Suttie, Janet L.
APPLICANT: Suttie, Janet L.
TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED TITLE OF INVENTION: SOUTH STATE MAIZE NUMBER OF SEQUENCES: 94
CORRESPONDENCE ADDRESS: 94
CORRESPONDENCE ADDRESS: 94
CORRESPONDENCE ADDRESS: 94
CORRESPONDENCE ADDRESS: 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: No. 6018104artis Corporation
STREET: Patent & Trademark Dept., 520 White Plains
STREET: Rd., POB 2005
CITY: Tracytown
STATE: New York
COUNTRY: USA
ZIP: 10591-9005
COMPUTER REABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM C compatible
COMPUTER: IBM C compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/459,595A FILING DATE: 02-JUN-1995 CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 22, Application US/08459595A Patent No. 6018104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     441 MIKEIDLDNDGKIDFSEFTAMMRKG 465
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FEATURE:
NAME/KEY: Protein
LOCATION: 1..464
COTHER INFORMATION: /note= "derived protein sequence of OTHER INFORMATION: pollen specific CDPK as disclosed in Figure 34."
US-08-459-595A-22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     309 GCLSEEBITGLKEMFKNIDKDNSGTITLDBLKHGLAKHGPKLSDSEMEKLMBAADADGNG 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        82 SEHPNVVRIKGTYEDSVFVHIVMEVCEGGELFDRIVSKGHFSERBAVKLIKTILGVVEAC 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              189 KYGPEADIWSVGVMLYIFLAGVPPFWAENENGIFTAILRGQLDLSSEPWPHISPGAKDLV 248
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    249 KKMLNINPKERLTAFQVLNHPWIKEDGDAPDTPLDNVVLDRLKQFRAMNQFKKAALRIIA 308
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            382 TIDYGEFLAATLHMNKMEREEILVAAFSDFDKDGSGYITIDELQSACTEFGLCDT-PLDD 440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             142 HSLGVMHRDLKPENFLFDSPKDDAKLKATDFGLSVFYKPGQYLYDVVGSPYYVAPEVLKK 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  202 CYGPEIDVWSAGVILYILLSGVPPFWAETESGIFRQILOGKLDFKSDPWPTISEAAKDLI 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              55.4%; Score 1437.5; DB 3; Length 464;
60.9%; Pred. No. 6.7e-112;
Live 70; Mismatches 103; Indels 1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      369 LIDYDEFVTATVHMNKLDREBHLYTAFQYFDKDNSGYITKEELEHALKEGGLYDADKIKD 428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22 LRDHYLLGKKLGQGQPGTTYLCTEKSTSANYACKSIPKRKLVCREDYEDVWREIQIMHHL 81
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/951,715

FILING DATE: 25.5EP-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/772,027

FILING DATE: 04.0CT-1991

ATTOMEN'APICATION NUMBER: US 07/772,027

NAME: Pace, Gary M.

REGISTRATION NUMBER: CGC 1577/CIP/DIV3

TELECOMMUNICATION INFORMATION:

TELEPRAX: (919) 541-8689

TELEPRAX: (919) 541-8689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     441 MIKEIDLDNDGKIDFSEFTAMMRKG 465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 60.9%
Matches 271; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 11
US-08-459-504B-22
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/note= "derived protein sequence of pollen specific CDPK as disclosed in Figure 34."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  69 $GQPNVVGLRGAYEDKQSVHLVMELCAGGELFDRIIARGQYTERGAAELLRAIVQIVHTC 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 55.4%; Score 1437.5; DB 3; Length 464; Best Local Similarity 60.9%; Pred. No. 6.7e-112; Matches 271; Conservative 70; Mismatches 103; Indels 1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9 VRATYSMGKELGRGQFGVTHLCTHRISGEKLACKTIAKRKLAAREDVDDVRREVQIMHHL 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22 LRDHYLLGKKLGQGQPGTTYLCTEKSTSANYACKSIPKRKLVCREDYEDVWREIQIMHHL 81
                                                                                                                                                                                                                                                                      APPLICANT: Suttie, Janet L.
TITLE OF INVENTION: SYMTHETIC DNA SEQUENCE HAVING ENHANCED
TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE
NUMBER OF SEQUENCES: 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,504B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CGC1577/CIP/DIV
                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: No. 6075185artis Corporation
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
PRIOR APPLICATION NUMBER: US 07/951,715
FILING DATE: 25-58F-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/772,027
FILING DATE: 04-007-1991
ATTONNEY ABOUT INFORMATION:
NAME: Maigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE DOCKET NUMBER: GGC1577/CIP
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION (919) 541-8577
TELECOMMUNICATION (919) 541-857
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
Kramer, Vance C.
Warren, Gregory W.
Brola, Stephen V.
Crossland, Lyle D.
Wright, Marcha S.
Marlin, Raren L.
Launis, Raren L.
Rochstein, Steven J.
Bowman, Cindy G.
Dawson, John L.
Dunder, Erik M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (919)541-8587
TELEPAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           464 amino acids
                                                                                                                                                                                                                                                     Pace, Gary M.
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                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION: 1..464
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amazza
STRANDEDNESS: sing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: Protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-459-504B-22
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APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: N
COUNTRY:
                                                                                                              APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
                                                                  APPLICANT:
APPLICANT:
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Sequence 22, Application US/08459504B
Petent No. 6075185
GENERAL INFORMATION
APPLICANT: Koziel, Michael G.
APPLICANT: Desai, Nalini M.
APPLICANT: Lewis, Kelly S.

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ADDRESSEE: No. 6320100artis Agribusiness Biotechnology Research, Inc.
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
as disclosed in Figure 34.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            249 KKMLNINPKERLTAFQVLNHPWIKEDGDAPDTPLDNVVLDRLKQFRAMNQFKKAALRIIA 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            322 BRLSEBEIGGLKELFKMIDTDNSGTITFEELKAGLKRVGSELMESEIKSLMDAADIDNSG 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       309 GCLSEEEITGLKEMFKWIDKDNSGTITLDELKHGLAKHGPKLSDSEMEKLMBAADADGNG 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                       69 SGQPNVVGLRGAYEDKQSVHLVMELCAGGELFDRIIARGQYTERGAAELLRAIVQIVHTC 128
                                                                                                                                                                                                                                                                                                                                                                                                                                SEHPNYVRIKGTYEDSVFVHIVMEVCEGGELFDRIVSKGHFSEREAVKLIKTILGVVEAC 141
                                                                                                                                                                                                                                                                                                                                                 22 LEDHYLLGKKLGQGQFGTTYLCTEKSTSANYACKSIPKRKLVCREDYEDVWREIQIMHHL 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HSLGVMHRDLKPENFLFDSPKDDAKLKATDFGLSVFYKPGQYLYDVVGSPYYVAPEVLKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                262 YKMLERSPKKRISAHEALCHPWIVDEQAAPDKPLDPAVLSRLKQFSQMNKIKKMALRVIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         382 TIDYGEFLAATLHWNKMEREEILVAAFSDFDKDGSGYITIDELQSACTEFGLCDT-PLDD
                                                                                                                                                                                                                                                                                                                                                                            9 VRATYSNGKELGRGQFGVTHLCTHRTSGEKLACKTIAKRKLAAREDVDDVRREVQIMHHL
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                                                                                                                                                                                                                                                                                                            ;
H
                                                                                                                                                                                                                                                                         Length
                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                         55.4%; Score 1437.5; DB 3; 60.9%; Pred. No. 6.7e-112; ive 70; Mismatches 103;
  pollen specific CDPK SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                            LOCATION: 1..464
SEQUENCE DESCRIPTION: SEQ ID NO: 22:
US-08-459-444-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Koziel, Michael G.
APPLICANT: Koziel, Malini M.
Lewis, Kally S.
Kramer, Vance C.
Warren, Gregory W.
Evola, Stephen V.
Crossland, Lyle D.
Wright, Martha S.
Merlin, Ellis J.
Launis, Karen L.
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Sequent No. 6320100
GENERAL INFORMATION:
                                         LENGTH: 464 amino acids
TYPE: amino acid
                                                                                STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 9.
                                                                                                                   MOLECULE TYPE: protein
HYPOTHETICAL: NO
FEATURE:
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                                                                                                   TOPOLOGY: linear
                                                                                                                                                                                                                                                                                               Best Local Similarity 60.9
Matches 271; Conservative
                                                                                                                                                                                NAME/KEY:
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US-09-547-422-22
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CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6121014artis Agribusiness Biotechnology Research, Inc.
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: NC
                                                                                                                                                                                                          ERLSEEEIGGLKELFKMIDTDNSGTITFEELKAGLKRVGSELMESEIKSLMDAADIDNSG 381
                                                                                                                                                                                                                                                                                       309 GCLSEEEITGLKEMFKNIDKDNSGTITLDELKHGLAKHGPKLSDSEMBKLMEAADADGNG 368
                                                                                                                                                                                                                                                                                                                                                                262 YKMLERSPKKRISAHBALCHPWIVDEQAAPDKPLDPAVLSRLKQFSOMNKIKKMALRVIA 321
                               HSLGVMHRDLKPENFLFDSPKDDAKLKATDFGLSVFYKPGQYLYDVVGSPYYVAPEVLKK 201
                                                     202 CYGPBIDVWSAGVILYILLSGVPPFWAETESGIFRQILQGKLDFKSDPWPTISEAAKDLI
                                                                                                                                                                                                                                                                                                                                           TIDYGEFLAATLHMNKMEREEILVAAFSDFDKDGSGYITIDELQSACTEFGLCDT-PLDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Crossland, Lyle D.
Wright, Martha S.
Merlin, Ellis J.
Launis, Earen L.
TITLE OF INVENTION: METHOD FOR PRODUCING A PLANT-OPTIMIZED
NUCLEIC ACID CODING SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOKET NUMBER: S-18805/P1/CGC1577/CIP/DIV6
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            뜅
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ZIP: 27709
COMPUTER READELE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,444A
PILING DATE: 02-Jun-1995
CLASSIFICATION: <UNKNOWN>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: /note= "derived protein sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 07/951,715
FILING DATE: 25-SEP-1992
APPLICATION NUMBER: US 07/772,027
FILING DATE: 04-OCT-1991
ATTORNEY/AGENT INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Koziel, Michael G.
Desai, Nalini M.
Lewis, Kelly S.
Kramer, Vance C.
Warren, Gregory W.
Evola, Stephen V.
                                                                                                                                                                                                                                                                                                                                                                                                                          MIKEIDLDNDGKIDFSEFTAMMRKG 465
                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 0, Application US/0845944A Patent No. 6121014 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (919)541-8689
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US-08-459-444-22
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FILING DATE: 25-SEP-1992
CLASSIFICATION: 800
PRICK APPLICATION DATA:
APPLICATION NUMBER: US 07/772,027
FILING DATE: 04-0CT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Spruill, W. Murray
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/951,715A
FILING DATE: 25-SEP-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CIBA-GEIGY Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                            Sequence 21, Application US/07951715A
Patent No. 5625136
GENERAL INFORMATION:
                  441 MIKEIDLDNDGKIDFSEFTAMMRKG 465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER: 32,94.
REPERENCE/DOCKET NUMBER: S.
TELECOMMUNICATION INFORMATION
TELEPHONE: (919)541-8615
                                                                                                                                                                                                                                                                                                        Crossland, Lyle D.
Wright, Martha S.
Merlin, Ellis J.
Launis, Karen L.
                                                                                                                                                                                      Koziel, Michael C
Desai, Nalini M.
Lewis, Kelly S.
                                                                                                                                                                                                                                                 Kramer, Vance C.
Warren, Gregory P
Evola, Stephen V.
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Bowman, Cindy G
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                                                                                                                                                                                                                                                                                                                                                                                                                        Dawson, John L.
Dunder, Erik M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 61.99
Matches 242; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7 Skyline Drive
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        , MOLECULE TYPE: protein US-07-951-715A-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: USA
ZIP: 10532
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: CIBA-GEIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
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CITY: Hawthorne
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                                                                                              RESULT 14
US-07-951-715A-21
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APPLICANT:
APPLICANT:
APPLICANT:
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INFORMATION FOR SEQ ID NO: /note= "derived protein sequence of
pollen specific CDFX as disclosed in Figure 34."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      249 KKMLNINPKERLTAFQVLNHPWIKEDGDAPDTPLDNVVLDRLKQFRAMNQFKKAALRIIA 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              322 BRLSEBEIGGLKELPKMIDTDNSGTITFEELKAGLKRVGSELMESEIKSLMDAADIDNSG 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      262 YKMLERSPKKRISAHBALCHPWIVDEQAAPDKPLDPAVLSRLKQFSOWKIKKMALRVIA 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    82 SEHPNYVRIKGTYEDSVFVHIVMEVCEGGELFDRIVSKGHFSEREAVKLIKTILGVVEAC 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         202 CYGPEIDVWSAGVILYILLSGVPPFWAETESGIFRQILQGKLDFKSDPWPTISEAAKDLI 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22 LRDHYLLGKKLGQGGFGTTYLCTEKSTSANYACKSIPKRKLVCREDYEDVWREIQIMHHL 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 60.9%; Pred. No. 6.7e-112;
Matches 271; Conservative 70; Mismatches 103; Indels 1;
                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/547,422
FILING DATE: 11-Apr-2000
CLASSIFICATION: <u >u
                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/459,595
FILING DATE: 02-UN-1995
APPLICATION NUMBER: US 07/951,715
FILING DATE: 25-SEP-1992
APPLICATION NUMBER: US 07/772,027
FILING DATE: 04-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, U, Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: S-18805H
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCATION: 1..464
; SEQUENCE DESCRIPTION: SEQ ID NO: 22:
US-09-547-422-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (919)541-8587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 464 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: Protein
                                                               COMPUTER READABLE FORM:
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MOLECULE TYPE: protein
HYPOTHETICAL: NO
                            COUNTRY: U
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APPLICANT: Suttie, Janet L. TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Patentin Release #1.0, Version #1.30B
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                                                                                             AAKDLIYKMLERSPKKRISAHEALCHPWIVDEQAAPDKPLDPAVLSRLKQFSQMNKIKKW 315
                                                                                                                                                                                                    ALRVIAERLSEEEIGGLKELFKMIDTDNSGTITFEELKAGLKRVGSELMESEIKSLMDAA 375
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QIVHTCHSMGVMHRDIKPENFLLLSKDEDAPLKATDFGLSVFFKEGELLRDIVGSAYYIA 120
                                                            PEVLKKCYGPEIDVWSAGVILYILLSGVPPFWAETESGIFRQILQGKLDFKSDPWPTISE 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Lanils, Marien L.
APPLICANT: Bowman, Cindy G.
APPLICANT: Bowman, Cindy G.
APPLICANT: Bowman, Cindy G.
APPLICANT: Bowman, Cindy G.
APPLICANT: Dawson, John L.
APPLICANT: Bowson, John L.
APPLICANT: Bowson, John L.
APPLICANT: Buttie, Janet L.
TITLE OF INVENTION: SYMTHETIC DNA SEQUENCE HAVING ENHANCED
TITLE OF INVENTION: SYMTHETIC DNA SEQUENCE HAVING ENHANCED
TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE
NUMBER OF SEQUENCES: 94
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 585936artis Corporation
STREET: Patent & Trademark Dept., 520 White Plains
STREET: Patent & Trademark Dept., 520 White Plains
STREET: New York
COUNTRY: USA
ZIP: 10591-9005
COUNTRY: USA
ZIP: 10591-9005
CONDUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION UNDER: US 07/951,715
FILING DATE: 25-SEP-1992
PROR APPLICATION NUMBER: US 07/772,027
PILING DATE: 25-SEP-1992
PROR APPLICATION NUMBER: US 07/772,027
ATTEND DATE: US-SEP-1992
PROR APPLICATION NUMBER: US 07/772,027
ATTEND DATE: US-SEP-1992
PROR APPLICATION NUMBER: US 07/772,027
ATTEND DATE: US-SEP-1992
ATTEND DATE:
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US-08-459-448A-21
Sequence 21, Application US/08459448A
Patent No. 5899336
GENERAL INFORMATION:
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Lewis, Kelly S.
Kramer, Vance C.
Evola, Stephen V.
Crossland, Lyle D.
Wright, Martha S.
Merlin, Ellis J.
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                                                                                                                                                                                                                                                                                                                                                                                                                        256 AAKDLIYKMLERSPKKRISAHEALCHPWIVDEQAAPDKPLDPAVLSRLKQFSQMNKIKKM
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                                                                                                                                                                                                                                                                                          Query Match

49.3%; Score 1277.5; DB 2; Length 408;
Best Local Similarity 61.9%; Pred. No. 1.2e-98;
Matches 242; Conservative 59; Mismatches 89; Indels 1;
     CGC 1577/CIP/DIV4
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REFERENCE/DOCKET NUMBER: CGC TELECOMUNICATION INFORMATION: TELEPHONE: (919)541-8582 TELEFRX: (919)541-8689 INFORMATION FOR SEQ ID NO: 21: SEQUENCE CHARACTERISTICS: LENGTH: 408 amino acids TYPE: amino acids
                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: protein
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SEQ ID NO 17
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                                                                                                                                                                            February 13, 2003, 21:11:33 ; Search time 19 Seconds (without alignments) 665.615 Million cell updates/sec
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Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-817-181-2
US-09-771-161A-188
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0 US-09-854-731-18

0 US-09-854-731-18

0 US-09-954-731-19

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US-09-992-481-4
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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ALIGNMENTS

ACKSIPKRKLVCREDYBDVWREIQIMHLSEHPNVVRIKGTYBDSVFVHIVMBVCEGGEL 112 PDRIVSKGHFSEREAVKLIKTILGVVEACHSLGVMHRDLKPENFLFDSPKDDAKLKATDF 172 240 FDRIVRRGHYTERKAAELARVIVGVVEACHSMGVMHRDLKPENFLFADHSBEAALKTIDF 299 173 GLSVFYKPGQYLYDVVGSPYYVAPEVLKKCYGPEIDVWSAGVILYILLSGVPPFWAETES 232 233 GIFRQILQGKLDFKSDPWPTISEAAKDLIYWMLERSPKKRISAHEALCHPWIVDEQAAPD 292 120 PSPRPRPQVKRVSSAGLLLGSVLRRKTENLKDKYSLGRRLGGGGFGTTHLCVERATGKEL 179 64.5%; Score 1672.5; DB 10; Length 639; 66.2%; Pred. No. 1.6e-110; tive 66; Mismatches 83; Indels 13; Gaps 5 PNPR-RPS-----NTVLPYQIPRLRDHYLLGKKLGQGQFGTTYLCTEKSTSANY 52 DB 10; Length 639; Sequence 17, Application US/09854731

Sequence 17, Application US/09854731

Patent No. US20020120949A1

PAPLICANT: Allen, Sreve

APPLICANT: Allen, Sreve

APPLICANT: Allen, Sreve

TITLE OF INVENTION: Plan Ming

FILE REFERRICE: BB-1171

CURRENT APPLICATION NUMBER: US/09/854,731

CURRENT FILING DATE: 2001-05-14

PRIOR APPLICATION NUMBER: 60/092,438

PRIOR FILING DATE: ANLY 10, 1998

NUMBER OF SEQ ID NOS: 23

SOFTWARE: Microsoft Office 97 Conservative Similarity TYPE: PRT CRGANISM: Zea mays US-09-854-731-17 Best Local Simi Matches 318;

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APPLICANT: COSTA e SILVA, OSWALDO DA
APPLICANT: COSTA e SILVA, OSWALDO DA
APPLICANT: COSTA e SILVA, OSWALDO DA
APPLICANT: BORNERT: HANS J.
APPLICANT: THIELEN, NOCHA VAN
APPLICANT: CHEN, ROUYING
APPLICANT: CHEN, ROUYING
APPLICANT: CHEN, ROUYING
TITLE OF INVENTION: PROTEIN KINASE STRESS-RELATED PROTEINS AND METHODS OF
TITLE OF INVENTION: USE IN PLANTS
TITLE OF INVENTION: USE IN PLANTS
FILE REFERENCE: 16313-0032
CURRENT APPLICATION NUMBER: US/09/928,313
CURRENT FILING DATE: 2000-04-06
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 128
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 39
LENGTH: 549
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                                                                                                                                                                                                                                                                                                 309 HIDFENDPWPKISNCAKDLVRKMLNPNVKIRLTAQQVLNHPWMKEDGDAPDVPLDNAVLT 368
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69 PRPKPASRSVSGVLGKPLSDIRQSYILGRELGRGQFGVTYLCTDKMYNBAYACKSIAKK 128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            249 DVFQDIVGSAYYVAPEVLKRSYGPEADVWSAGVIVYILLCGVPPFWAETEQGIFDAVLKG 308
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                                                                         293 KPLDPAVLSRLKQFSQMNKIKKMALRVIAERLSEEEIGGLKELFKMIDTDNSGTITFEEL 352
                                                                                                                                                                                                                                                                    413 KDGSGYITIDELQSACTEFGLCDTPLDDMIKEIDLDNDGKIDFSEFTAMMRKGDGVGRSR 472
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 10; Length 549;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 58.2%; Score 1509.5; DB 10; Length Best Local Similarity 60.8%; Pred. No. 4.1e-99; Matches 290; Conservative 70; Mismatches 112; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 39, Application US/09828313
Patent No. US20020059662A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ) TYPE: PRT
; ORGANISM: Physcomitrella patens
US-09-828-313-39
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US-09-828-313-39
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APPLICANT: COSTA & SILVA, OSWALDO DA APPLICANT: COSTA & SILVA, OSWALDO DA APPLICANT: COSTA & SILVA, OSWALDO DA APPLICANT: THIELEN, NOCHA VAN APPLICANT: THIELEN, NOCHA VAN APPLICANT: CHEN, ROUYING; APPLICANT: CHEN, RODRIGO; TITLE OF INVENTION: USE IN PLANTS

FILE REFERENCE: 16313-0032

CURRENT APPLICATION NUMBER: US/09/828,313

CURRENT APPLICATION NUMBER: 60/196,001

PRIOR APPLICATION NUMBER: 60/196,001

PRIOR APPLICATION NUMBER: 60/196,001

NUMBER OF SEQ ID NOS: 128

SEQ ID NO 38

SEQ ID NO 38
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Best Local Similarity 36.9%; Pred. No. 1.7e-52;
Matches 203; Conservative 92; Mismatches 163; Indels 92; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    122 BAVDGEKPLDKHFGYHKNPATKYELGHEVGRGHFGHT--CYAKVRKGEHKGQAVAVKIIS 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 59 KRKLVCREDYEDVWREIQIMHHLSEHPNVVRIKGTYEDSVFVHIVMEVCEGGELFDRIVS 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    180 KAKMITAIAIEDVGREVKILKALIGHQNLVRFYDSCEDHLNVXIVMELCEGGELLDRILS 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             119 K-GHFSEREAVKLIKTILGVVEACHSLGVMHRDLKPENFLFDSPKDDAKLKATDFGLSVF 177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             238 ILQGKLDFKSDPWPTISBAAKDLIYKMLERSPKKRISAHBALCHPWIVDEQAAPDKPLDP 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 298 AVLSRIKQFSQMNKIKKWALRVIAERISBEBIGGIKELFKMIDTDNSGTITFBELKAGIK 357
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             478 KNSTEAMKESRVFEILESMÖGLHFKKMDFSEFCAAAISVLQLEATERWEQHARAAYDIFE 537
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22 -----LRDH-----ACKSIP 58
                             422 DELQSACTEFGLCD-TPLDDMIKEIDLDNDGKIDPSEFTAMMRKGD-GVGRSRTMMK 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5 PNPRRPSNIVLPY-----QIPR----
                                                                                                                                                                                        Sequence 38, Application US/09828313 Patent No. US20020059662A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT ; ORGANISM: Physcomitrella patens US-09-828-313-38
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         174 YDLGKEVGRGHFGHTCSAVVKKGEHKGHTVÅVKIİSKAKMTTAISIEDVRREVKİLKALS 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                83 EHPNVVRIKGTYEDSVFYHIVMEVCEGGELFDRIVSK-GHFSEREAVKLIKTILGVVEAC 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     142 HSLGVMHRDLKPENFLFDSPKDDAKLKATDFGLSVFYKPGQYLYDVVGSPYYVAPEVLKK 201
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                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                          26 YLLGKKLGQGQFGTTYLCTEKS---TSANYACKSIPKRKLVCREDYEDVWREIQIMHHLS 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      202 CYGPEIDVWSAGVILYILLSGVPPFWAETESGIFRQILQGKLDFKSDPWPTISEAAKDLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         381 GTIDYGEFLAATL---HMNKMER-EEILVAAFSDFDKDGSGYITIDFLQSACTEFGLCDT
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                                                                                                                                                                                                                                                                    Length 625;
                                                                                                                                                                                                                                                                        31.9%; Score 826; DB 10; Length 62
40.8%; Pred. No. 7.3e-51;
tive 85; Mismatches 159; Indels
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APPLICANT: Allen, Steve
APPLICANT: Lee, Jian Ming
TITLE OF INVENTION: Plant Protein Kinases
FILE REFERENCE: BB-1171
CURRENT APPLICATION NUMBER: US/09/854,731
CURRENT FILING DATE: 2001-05-14
PRIOR PREDICATION NUMBER: 60/022,438
PRIOR PILING DATE: July 10, 1998
NUMBER OF SEQ ID NOS: 23
SOFTWARE: Microsoft Office 97
SEQ ID NO 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : | | : : | | : : | | | : | 588 HYSIVQDWIRK----SDGKLNFLGFTKFL 612
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; ORGANISM: Arabidopsis thaliana
US-09-854-731-19
NUMBER OF SEQ ID NOS: 23
SOFTWARE: Mcrosoft Office 97
SEQ ID NO 18
LENGTH: 625
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Best Local Similarity 38.1%
Matches 177; Conservative
                                                                                                                                                                                                                                                                                                                                                  Matches 183; Conservative
                                                                                                                                                                                                                                                                                                                 Best Local Similarity
                                                                                                                                  ; TYPE: PRT
; ORGANISM: Zea mays
US-09-854-731-18
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Sequence 18, Application US/09854731
Patent No. US20020120949A1
Sequence 18, Application US/09854731
Patent No. US20020120949A1
TERENT PATENT Allen, Steve
TITLE OF INVENTION: Plan Ming
TITLE OF INVENTION: Plan Protein Kinases
FILE REFERENCE: BB-1171
CURRENT APPLICATION NUMBER: US/09/654,731
CURRENT FILING DATE: 2001-05-14
PRIOR FILING DATE: July 10, 1998
                                                                                                                                     Sequence 4, Application US/09854731
Patent No. US20020120949A1
GENERAL INFORMATION: Steve
APPLICANT: Allen, Steve
APPLICANT: Lee, Jian Ming
TITLE COF INVENTION: Plant Protein Kinases
FILE REFERENCE: BB-1171
CURRENT APPLICATION NUMBER: US/09/854,731
CURRENT FILING DATE: JO01-05-14
PRIOR APPLICATION NUMBER: 60/092,438
FRIOR APPLICATION NUMBER: 60/092,438
FRIOR FILING DATE: JULY 10, 1998
NUMBER OF SEQ ID NOS: 23
SOFTWARE: Microsoft Office 97
SEQ ID NO 4
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Best Local Similarity 40.6%
Matches 183; Conservative
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US-09-854-731-4
                                                                                     RESULT 4
US-09-854-731-4
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Sequence 4, Application US/09817181
Sequence 4, Application US/09817181
Sequence 4, Application US/09817181
Sequence 4, Application US/09817181
Sequence 4, Application US/09817181
Sequence 4, Application US/09817181
APPLICANT: MERKULOW: Gennady et al APPLICANT: MISCARTION: ACID MULECULES ENCODING HUMAN KINASE PROTEINS, AND USES TITLE OF INVENTION: THEREOF TITLE OF INVENTION: THEREOF TITLE OF INVENTION: THEREOF US/09/817,181
CURRENT APPLICATION NUMBER: US/09/817,181
CURRENT PLING DATE: 2001-03-27
NUMBER OF SEQ ID NOS: 4
SEQ ID NO 4
SEQ ID NO 4
SEQ ID NO 4
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                                     239 AKDFIRHLMEKDPEKRFTCEQALQHPWIAGDTAL-DKNIHQSVSEQIKKNFAKSKWKQ 295
257 AKDLIYKMLERSPKKRISAHEALCHPWIVDEQAAPDKPLDPAVLSRLKQFSQMNKIKK 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12 QAEDIRDIYDFRDVLGTGAFSEVILAEDKRTQKLVAIKCIAKEALEGKEG--SMENETAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22.7%; Score 587.5; DB 10; Length 370; 41.6%; Pred. No. 2.5e-34; tive 55; Mismatches 114; Indels 5;
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TITLE OF INVENTION: 68730 and 69112, Protein Kinase

TITLE OF INVENTION: 68730 and 69112, Protein Kinase

TITLE OF INVENTION: MODECULES and Uses Therefor

FILE REPERENCE: MPI2000-521P1R (M)

CURRENT PILING DATE: 2001-12-17

PRIOR FILING DATE: 2001-12-17

PRIOR FILING DATE: 2001-12-22

NUMBER OF SEQ ID NOS: 10

SEQ ID NO S: 50 TO NOS: 10
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Pred. No. 5.5e-32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; sequence 2, Application US/10024036B; Publication No. US20030028004A1; GENERAL INFORMATION:
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37.1%;
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TYPE: PRT
ORGANISM: Homo sapiens
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Best Local Similarity
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Matches 124;
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; Sequence 36, Application US/09935464
; Sequence 36, Application No. US20030027153A1
; GENERAL INFORMATION:
    APPLICANT: Meyer, Joanne
    APPLICANT: Barrington-Martin, Rory
    APPLICANT: Barrington-Martin, Rory
    APPLICANT: Parker, Alexander
    TITLE OF INVENTION: MITHORS AND COMPOSITIONS FOR DIAGNOSING AND TREATING NEURING PILLE OF INVENTION: DISORDERS SUCH AS SCHIZOPHRENIA
    TITLE OF INVENTION: DISORDERS SUCH AS SCHIZOPHRENIA
    FILE REPERENCE: 3322/14702 US:
    CURRENT APPLICATION NUMBER: US/09/935, 464
    CURRENT APPLICATION NUMBER: US 09/757,300
    PRIOR APPLICATION NUMBER: US 09/757,300
    PRIOR FILING DATE: 2001-01-09
    NUMBER OF SEQ ID NOS: 90
    SOFTWARE: Patentin version 3.0
    SEQ ID NO 36
    LENGTH: 317
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                                                                                                                                                                                                                                                                                                                                                                           378 DNSGTIDYGEFLAATLHMNKMER----EEILVAAFSDFDKDGSGYITIDELQSACTEFGL 433
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                                                                                                                                                                                                                                                                                                                                             DLIYKMLERSPKKRISAHEALCHPWIVDEQAAPDKPLDPAVLSRLKQFSQMNKIKKMALR 318
                                                                                                                                                                                                                                                                                                                                                                                                                                           319 VIAERLSEEBIGGLKELFKMIDTDNSGTITFEELKAGLKRVGSELM-ESEIKSLMDAADI 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18 OTPRIRDHYLLGKKIGGGGFGTTYLCTEKSTSANYACKSIPKRKLVCREDYEDVWREIQI 77
                                                                                                                                                                                                                                          LKKCYGPEIDVWSAGVILYILLSGVPPFWAETESGIFRQILQGKLDFKSDPWPTISEAAK 258
                                          HLSEHPNVVRIKGTYEDSVFVHIVMEVCEGGELFDRIVSK-GHFSEREAVKLIKTILGVV
                                                                                                                                                                          240 AYCHLQGVVHRDLKPENFEFSTKDETSPLKAIDFGLSDYVKPDERLNDIVGSAYYVAPEV
                                                                                                                                                                                                                                                                                           300 LHRTYGTBADMWSIGVIAVILLCGSRPFWARTESGIFRAVLKAEPNFEBAPWPSLSPBAV
                                                                          139 BACHSLGVMHRDLKPENFLFDSPKDDAKLKATDFGLSVFYKFGQYLYDVVGSPYYVAPEV
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CRGANISM: Homo sapiens
US-09-935-464-36
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Matches 124;
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US-09-935-464-3
US-09-935-464-3
Sequence 3, Application US/09935464
Publication No. US20030027153A1
GENERAL INFORMATION:
APPLICANT: Meyer, Joanne
APPLICANT: Barrington-Martin, Rory
APPLICANT: Barrington-Martin, Rory
APPLICANT: Parker, Alexander
TITLE OF INVENTION: DISORDERS SUCH AS SCHIZOPHRENIA
FILE REPREBUGE: 3322/14702 US1
CURRENT APPLICATION NUMBER: US/09/935,464
CURRENT APPLICATION NUMBER: US/09/935,464
CURRENT APPLICATION NUMBER: US/09/935,7300
PRIOR FILING DATE: 2001-01-09
NUMBER OF SEQ ID NOS: 90
SOFTWARE: Patentin version 3.0
SEQ ID NO 3
SEQ ID NO 3
SEQ ID NO 3
SEQ ID NO 3
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APPLICANT: Merrin, Rory
APPLICANT: Merrin, Rory
APPLICANT: Merrin, Rory
APPLICANT: Merrinon-Martin, Rory
APPLICANT: Merrinon: Methods And compositions for diagnosting and treating neuropsychip
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND TREATING NEUROPSYCHIP
TITLE OF INVENTION: DISORDESS SUCH AS SCHIZOPHRENIA
TITLE OF INVENTION: DISORDESS SUCH AS SCHIZOPHRENIA
TITLE OF INVENTION: DISORDESS SUCH AS SCHIZOPHRENIA
CURRENT APPLICATION NUMBER: US 09/757,300
PRIOR PRIOR PRILICATION NUMBER: US 09/757,300
PRIOR FILING DATE: 2001-01-09
NUMBER OF SEQ ID NOS: 90
SOFTWARE: Patentin version 3.0
SEQ ID NO SEQ ID NO SEQ ID NOS: 476
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                                                 307 IMLVSRNFSAAKSLLNKKSDGGVK 330
319 VI-----AERLSEEFIGGLK 333
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Best Local Similarity 39.6'
Matches 116; Conservative
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US-09-935-464-3
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US-09-935-464-5
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APPLICANT: YE, Jane et al.
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
TITLE OF INVENTION: THEREOF
FILE REPREMENCE: CLOOLISSOIV
CURRENT APPLICATION NUMBER: US/10/096,960
CURRENT APPLICATION NUMBER: 09/800,960
PRIOR PRIOR PLING DATE: 2001-03-08
NUMBER OF SEQ ID NOS: 4
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                                                                                                                                                                                                                                                                                                                                                                  SAGVILYILLSGVPPFWAETESGIFRQILQGKLDFKSDPWPTISEAAKDLIYKWLERSPK 270
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         92 GTYEDSVFVHIVMEVCEGGELFDRIVSKGHFSEREAVKLIKTILGVVEACHSLGVMHRDL 151
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                                                                                                   29 LGTGAFSEVVLAEEKATGKLFAVKCIPKKALKGKE--SSIENEIAVLRKI-KHENIVALE 85
                                                    LGQGQFGTTYLCTEKSTSANYACKSIPKRKLVCREDYEDVWREIQIMHLSEHPNVVRIK 91
                                                                                                                                                                                      13;
     12;
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     66; Mismatches 120; Indels
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Matches 120; Conservative
     Conservative
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US-10-096-960-4
     Matches 117;
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) ORGANISM: Human
US-09-817-181-2
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US-09-771-161A-188
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TYPE: PRT
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Patent No. US20020132325A1
CENERAL INFORMATION:
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TITLE OF INVENTION:
COLOR INVENTION:
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CURRENT APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                             190 VLAOKPYSKAVDCWSIGVITYÍLLCGYPPRYEBTÉSKLFBKÍKBGYYBFBSPFWDDÍSES 249
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                                                                                                                                                         Gaps
                                                                                                                                                                                                                     18 OTPRIRDHYLLGKKIGOGOFGTTYLCTEKSTSANYACKSIPKRKLVCREDYEDVWREIQI 77
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                                                                                       Length 476;
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20.8%; Score 539; DB 12; Length 5
Best Local Similarity 39.0%; Pred. No. 1.1e-30;
Matches 115; Conservative 58; Mismatches 118; Indels
                                                                                       Query Match
20.9%; Score 543; DB 9; Length 47
Best Local Similarity 39.6%; Pred. No. 4.7e-31;
Matches 116; Conservative 62; Mismatches 107; Indels
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SOSTWARE: FastSEQ for Windows Version 4.0
SEQ ID NUMBER SES
LENGTH: 565
; ORGANISM: Homo sapiens
US-09-935-464-5
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; ORGANISM: Homo sapien
US-10-096-960-2
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Sequence 2, Application US/09817181

Sequence 2, Application US/09817181

Sequence 2, Application US/09817181

GENERAL INFORMATION:

APPLICANT: MERKULOW, Gennady et al

APPLICANT: MERKULOW, Gennady et al

TITLE OF INVENTION: THEREOF

TITLE OF INVENTION: THEREOF

TITLE OF INVENTION: THEREOF

FILE REPERBYCE: CL000189

CURRENT APPLICATION NUMBER: US/09/817,181

CURRENT FILING DATE: 2001-03-27

NUMBER OF SEQ ID NOS: 4

SEQ ID NO 2.

SEQ ID NO 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           87; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
20.8%; Score 538.5; DB 10;
Best Local Similarity 42.8%; Pred. No. 6.1e-31;
Matches 107; Conservative 53; Mismatches 87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INVERSION:
GENERAL INVERSION:
TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES
FILE REFERENCE: 802260-2005.1
FILE REPERSINGE: 802260-2005.1
CURRENT APPLICATION NUMBER: U8/09/771,161A
CURRENT FILING DATE: 2001-0.26
PRIOR APPLICATION NUMBER: 136776
PRIOR FILING DATE: 2000-06-15
PRIOR FILING DATE: 2000-06-15
PRIOR FILING DATE: 2000-04-12
NUMBER OF SEQ ID NOS: 273
SOFTWARE: PATCHIN VENSION 3.0
SEQ ID NO 188
LENGTH: 387
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Pred. No. 1.7e-30;
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Best Local Similarity
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202	254	258	310	303		
143 SLGWMHRDLKVENFLFDSPKDDAKLKATDFGLSVFYKDGQYLYDVVGSPYYVABEVLKKC 202 ::	203YGPEIDVWSAGVILYILLSGVPFWAETESGIFRQILQGKLDFKSDPWFTIS 254) SMNEDHPGYGKEVDMMSTGVÍMYTLÍLAGSPPFWHRKQMLMLRMIMSGNYQFGSPEWDDYS	255 BAAKDLIYKMLERSPKKRISAHEALCHPWIVDEQAAPDKPLDPAVLSRLKQFSQMN 310	DIVKDLVSRFLVVQPQNRYTABEALAHPFFQQYLVBEVRHFSPRG	311 KIKKMALRVIA 321	- 124
143	203	199	255	259	311	304
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Matches 115; Conservative 53; Mismatches 100; Indels 43; Gaps

Search completed: February 13, 2003, 21:18:42 Job time : 20 secs

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                                                                                   February 13, 2003, 21:04:42; Search time 38 Seconds (without alignments) 1252.277 Million cell updates/sec
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2593
1 METKPNPRRPSNTVLPYQTP.......KNLNFNIADAFGVDGEKSDD 495
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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                  Total number of hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
                                                          - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Match Length DB
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1458.5
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T10938	H86322	S46283	F96776	T02139	F85059	T46189	817759	S71778	C84774	A84847	E84721	C85059	T51156	S54788	T00835
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(S) Superfamily: calcium-dependent protein kinase, calmodulin repeat homology, protein kinase, csymords: ATP: calcium binding; EF hand; phosphotransferase, serine/threonine-specificyeywords: ATP: calcium binding; EF hand; phosphotransferase, serine/threonine-specificy22-282/bomain: protein kinase homology «KIN»

F;30-38/Region: protein kinase ATP-binding motif
F;34-38/Region: calmodulin repeat homology «EFH»
F;34-356/Domain: calmodulin repeat homology «EFH»
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calcium-dependent protein kinase (EC 2.7.1.-) - soybean
calcium-dependent protein kinase (EC 2.7.1.-) - soybean
C;Species: Clycine max (soybean)
C;Date: 03.Mar-1993 #sequence_revision 14-Jul-1994 #text_change 11-Jun-1999
C;Accession: A43713
R;Harper, J.*F; Sussman, M.R.; Schaller, G.E.; Putnam-Evans, C.; Charbonneau, Science 252, 951-954, 1991
A;Title: A calcium-dependent protein kinase with a regulatory domain similar
                                                                                                                                                            calcium-dependent protein kinase (EC 2.7.1.-) beta - soybean calcium-dependent protein kinase (EC 2.7.1.-) beta - soybean C.Species: Glycine max (soybean)
C.bate: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jan-2000 C.Accession: T08873
E.ide, J.Y.; Yoo, B.C.; Harmon, A.C. submitted to the EMBL Data Library, September 1996
A.Accession: T08873
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1e-68;
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81.1%; Pred. No. 1e-6
ive 43; Mismatches
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EAFGVEDTSSTAKSDD 498
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Matches 386; Conserv
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Accession: G85097
R;anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Sprin Rautre 402, 769-777, 1999
A;Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana. A;Accession: G85097
A;Accession: G85097
A;Accession: G85097
A;Accession: C85097
A;Accessi
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C;Superfamily: calcium-dependent protein kinase; calmodulin repeat homology; protein
C;Keywords: EF hand
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      SRLKQFSQMNKIKKWALRVIAERLSEEIGGLKELFKMIDTDNSGTITFEELKAGLKRVG 360
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                                                                                                                    361 SELMESEIKSLWDAADIDNSGTIDYGEFLAATLHWNKMEREEILVAAFSDFDKDGSGYIT
                                                                                                                                                                                          421 IDELQSACTEFGLCDTPLDDMIKEIDLDNDGKIDFSEFTAMMRKGDGVGRSRTWMKNINF
                                                                      SELMESEIKSLMDAADIDNSGTIDYGEFLAATLHMNKWEREEILVAAFSDFDKDGSGYIT
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Pred. No. 1.6e-84;
9; Mismatches 13;
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ilarity 94.8%;
Conservative
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Matches 470;
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A; Recented the times: 3/1137, A; Recession: $7130.

A; Recented the type: DNA
A; Residues: 1-164, S', 166-239, E', 241-300, KF', 303-350, S', 352-490 <HOW>
A; Residues: 1-164, S', 166-239, E', 241-300, KF', 303-350, S', 352-490 <HOW>
A; Residues: 1-164, S', 166-239, E', 74 Chye, M.L.; Tan, C.T.; Koh, C.C.; Chua, N
R; Hong, Y.; Takano, M.; Liu, C.M.; Gasch, A.; Chye, M.L.; Tan, C.T.; Koh, C.C.; Chua, N
R; Hong, Y.; Takano, M.; Liu, C.M.; Gasch, A.; Chye, M.L.; Tan, C.T.; Koh, C.C.; Chua, N
A; Description: Expression of the calcium dependent protein kinase gene family in Arabidc
A; Reference number: $71196
A; Reference number: $71196
A; Residues: 1-164, S', 166-239, E', 241-300, KF', 303-350, S', 352-490 <HOA>
A; Residues: 1-164, S', 166-239, E', 241-300, KF', 303-350, S', 352-490 <HOA>
A; Residues: 1-164, S', 166-239, E', 241-300, KF', 303-350, S', 352-490 <HOA>
A; Residues: 1-164, S', 166-239, E', 241-300, KF', 303-350, S', 352-490 <HOA>
A; Residues: 1-164, S', 166-239, E', 241-300, KF', 303-350, S', 352-490 <HOA>
A; Residues: 1-164, S', 166-239, E', 241-300, KF', 303-350, S', 352-490 <HOA>
A; Residues: 1-164, S', 166-239, E', 241-300, KF', 303-350, S', 352-490 <HOA>
A; Residues: 1-164, S', 166-239, E', 241-300, KF', 303-350, S', 352-490 <HOA>
A; Residues: 1-164, S', 166-239, E', 241-300, KF', 303-350, S', 352-490 <HOA>
A; Residues: 1-164, S', 166-239, E', 241-300, KF', 303-350, S', 352-490 <HOA>
A; Residues: 1-164, S', 166-239, E', 241-300, KF', 303-350, S', 352-490 <HOA>
A; Residues: 1-164, S', 166-239, E', 241-300, KF', 303-350, S', 352-490 <HOA>
A; Residues: 1-164, S', 166-239, E', 241-300, KF', 303-350, S', 352-490 <HOA>
A; Residues: 1-164, S', 166-239, E', 241-300, KF', 303-350, S', 352-490 <HOA>
B; Residues: 1-164, S', 166-239, E', 241-300, KF', 303-350, S', 352-490 <HOA>
B; Residues: 1-164, S', 166-239, E', 241-300, KF', 303-350, S', 352-490 <HOA>
B; Residues: 1-164, S', 166-239, E', 241-300, KF', 303-350, S', 352-490 <HOA>
B; Residues: 1-164, S', 166-239, E', 241-300, S', 333-350, S', 333-350, S', 332
                      Arabido
e EMBL Data Library, February 1995
Expression of the calcium-dependent protein kinase gene family in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HFSEREAVKLIKTILGVVEACHSLGVMHRDLKPENFLFDSFKDDAKLKATDFGLSVFYKP 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
71.2%; Score 1847.5; DB 1;
Best Local Similarity 73.5%; Pred, No. 5.6e-62;
Matches 355; Conservative 52; Mismatches 69; I
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C;Species: Zea mays (maize)
                              A, Description: Expression of Reference number: 871197
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                              A,Accession: A43713
A,Accession: A43713
A,Molecule type: mRNA
A,Molecule type: mRNA
A,Molecule type: mRNA
A,Molecule type: mRNA
A,Molecule: 1-508 cHAR>
A,Cross-references: EMBL:M64987; NID:g169930; PIDN:AAB00806.1; PID:g169931
A,Cross-references: EMBL:M64987; NID:g169930; PIDN:AAB00806.1; PID:g169931
C,Superfamily: calcium dependent protein kinase homology cKIN>
F,32-292/Domain: protein kinase homology cKIN>
F,32-392/Domain: calmodulin repeat homology cER>
F,335-367/Domain: calmodulin repeat homology cRF>
F,401-493/Domain: calmodulin repeat homology cRF>
F,401-473/Domain: calmodulin repeat homology cRF4>
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C;Date: 14-May-1999 #sequence revision 14-May-1999 #text_change 18-Jun-1999
C;Accession: 571776; S71776; S71902; S711902; S71190; M.L.; Chua, N.H.
Piant Mol. Biol. 30, 1259-1275, 1996
A;Title: Expression of three members of the calcium-dependent protein kinase A;Teference number: 571774; MUID:96311013; PMID:8704134
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                                                                                                                                                                                                                                                                                                                                                                    Length 508,
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          Reference number: A43713; MUID:91240279; PMID:1852075
                                                                                                                                                                                                                                                                                                                                                                    75.0%; Score 1944; DB 1; 77.7%; Pred. No. 1.6e-65; iive 51; Mismatches 51;
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Hong, Y.; Takano, M.; Liu, C.M.; Gasch,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            shown
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A,Accession: S71775
A,Status: nucleic acid sequence not
A,Molecule type: mRNA
A,Robecules: 1-490 <40F>
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A;Molecule type: DNA
A;Residues: 1-490 <HON>
                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 77.7%
Matches 370; Conservative
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Length 487;

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A;Molecule type: mRNA
A;Residues: 1-497 <BOTS
A;Residues: 1-497 <BOTS
A;Residues: 1-497 <BOTS
A;Cross-references: EMEL:U08140; NID:g967124; PIDN:AAC49405.1; PID:g967125
A;Cross-references: Extain Rwilcz, cv. Berken, clone pVr-CDPK-1
C;Superfamily: calcium-dependent protein kinase; calmodulin repeat homology; protein kinase C;Keywords: ATP; calcium-dependent protein kinase posphotransferase; serine/threonine-specific F;30-38/Region: protein kinase ATP-binding motif F;32-38/Region: protein kinase ATP-binding motif F;35-357/Domain: calmodulin repeat homology <BE2>
F;351-393/Domain: calmodulin repeat homology <BF3>
F;341-463/Domain: calmodulin repeat homology <BF8>
F;31-463/Domain: calmodulin repeat homology <BF8>
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                                                                                                                                                                                                                                                                                                                                                                                                      Query Match

Best Local Similarity 69.1%; Pred. No. 2e-58;

Matches 327; Conservative 64; Mismatches 80; Indels
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                               Cyacession: 19271

RyBerberich, T.; Kusano, T.

RyBerberich, T.; Kusano, T.

RyBerberich, T.; Kusano, T.

RyTitle: Cycloinaximide induces a subset of low temperature-inducible genes in maize.

A;Title: Cycloinaximide induces a subset of low temperature-inducible genes in maize.

A;Reference number: 214973

A;Reference number: 214973

A;Ratus: translated from GB/EMBL/DDBJ

A;Ratus: translated from GB/EMBL/DDBJ

A;Rossidues: 1-492 ABBR.

A;Rossidues: 1-492 ABBR.

A;Rossidues: 1-492 ABBR.

A;Rossidues: 1-492 ABBR.

A;Rossidues: 1-492 ABBR.

A;Rossidues: GBRU: DB4408; PIDN:BAA12338.1

A;Rossidues: 1-492 ABBR.

A;Rossidues: GBRU: DB408; PIDN:BAA12338.1

A;Rossidues: GBRU: DB409 ABBR.

A;Rossidues: GBRU: GBRU: GBRU: GBRU: GBRU: GBRU: GBRU: GBRU: GBRU: GBRU: GBRU: GBRU: GBRU: GBRU: GBRU: GBRU: GBRU: GBRU: GBRU: GBRU: GBRU: GBRU: GBRU: GBRU: GBRU: GBRU: GBRU: GBRU: GBRU: GBRU: GBRU: GBRU: GBRU: GBRU: GBRU: GBRU: GBRU: GBRU: GBRU: GBRU: GBRU: GBRU: GBRU: GBRU: GBRU: GBRU: GBRU: GBRU: GBRU: GBRU: GBRU: GBRU: GBRU: GBRU: GBRU: GBRU: GBRU: GBRU: GBRU: GBRU: GBRU: GBRU: GBRU: GBRU: GBRU: GBRU: GBRU: GBRU: GBRU: GBRU: GBRU: GBRU: GBRU: GBRU: GBRU: GBRU: GBRU: GBRU: GBRU: GBRU: GBRU: GBRU: GBRU: GBRU: GBRU: GBRU: GBRU: GBRU: GBRU: GBRU: GBRU: GBRU: GBRU: GBRU: GBRU: GBRU: GBRU: GBRU: GBRU: GBRU: GBRU: GBRU: GBRU: GBRU: GBRU: GBRU: GBRU: GBRU: GBRU: GBRU: GBRU: GBRU: GBRU: GBRU: GBRU: GBRU: GBRU: GBRU: GBRU: GBRU: GBRU: GBRU: GBRU: GBRU: GBRU: GBRU: GBRU: GBRU: GBRU: GBRU: GBRU: GBRU: GBRU: GBRU: GBRU: GBRU: GBRU: GBRU: GBRU: GBRU: GBRU: GBRU: GBRU: GBRU: GBRU: GBRU: GBRU: GBRU: GBRU: GBRU: GBRU: GBRU: GBRU: GBRU: GBRU: GBRU: GBRU: GBRU: GBRU: GBRU: GBRU: GBRU: GBRU: GBRU: GBRU: GBRU: GBRU: GBRU: GBRU: GBRU: GBRU: GBRU: GBRU: GBRU: GBRU: GBRU: GBRU: GBRU: GBRU: GBRU: GBRU: GBRU: GBRU: GBRU: GBRU: GBRU: GBRU: GBRU: GBRU: GBRU: GBRU: GBRU: GBRU: GBRU: GBRU: GBRU: GBRU: GBRU: GBRU: GBRU: GBRU: GBRU: GBRU: GBRU: GBRU: GBRU: GBRU: GBRU: GBRU: GBRU: GBRU: GBRU: GBRU: GBRU: GBRU: GBRU: GBRU: GBRU: GBRU: GBRU: GBRU: GBRU: GBRU: GBRU: 
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         14-May-1999 #sequence_revision 14-May-1999 #text_change 16-Jun-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    67.6%; Score 1752; DB 1; Length 492; illarity 70.6%; Pred. No. 1.9e-58; Conservative 54; Mismatches 83; Indels
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Matches 334; Conserv
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193 191 373 371 431

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calcium-dependent protein kinase (EC 2.7.1.-) 7 - maize
calcium-dependent protein kinase (EC 2.7.1.-) 7 - maize
C;Species: Zea mays (maize)
C;Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change 21-Jul-2000
C;Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change 21-Jul-2000
C;Date: 1703263
R;Satio, Y: Hata, S: Sheen, J: Izui, K.
Biochim. Biophys. Acta 1350, 109-114, 1997
A;Ttele: CDNA cloning and prokaryotic expression of a maize calcium-dependent protein k
A;Reference number: Z14815; MUID:97201047; PMID:9048876
A;Reference number: Z14815; MUID:97201047; PMID:9048876
A;Reference number: Z14815; MUID:97201047; PMID:9048876
A;Reference number: Z14815, MUID:97201047; PMID:9048876
A;Residues: Translated from GB/EMBL/DDBJ
A;Residues: 1-554 «SAI»
A;Residues: 1-554 «SAI»
A;Cross-references: EMBL:D87042; NID:g1504051; PIDN:BAA13232.1; PID:g1504052
A;Residues: 1-554 «SAI»
A;Cross-references: EMBL:D87042; NID:g1504051; PIDN:BAA13232.1; PID:g1504052
A;Cross-references: EMBL:D87042; NID:g1504051; PIDN:BAA13232.1; PID:g1504052
A;Cross-references: EMBL:D87042; NID:g1504051; PIDN:BAA13232.1; PID:g1504052
A;Cross-references: EMBL:D87042; NID:g1504051; PIDN:BAA13232.1; PID:g1504052
A;Cross-references: EMBL:D87042; NID:g1504051; PIDN:BAA13232.1; PID:g1504052
A;Cross-references: EMBL:D87042; NID:g1504051; PIDN:BAA13232.1; PID:g1504052
A;Cross-references: EMBL:D87042; NID:g1504051; PIDN:BAA13232.1; PID:g1504052
A;Cross-references: EMBL:D87042; NID:g1504051; PIDN:BAA13232.1; PID:g1504052
A;Cross-references: EMBL:D87042; NID:g1504051; PIDN:g1504052
A;Cross-references: EMBL:D87042; NID:g1504051; PIDN:g1504052
A;Cross-references: EMBL:D87042; NID:g1504051; PIDN:g1504052
A;Cross-references: EMBL:D87042; NID:g1504051; PIDN:g1504052
A;Cross-references: EMBL:D87042; NID:g1504052; PIDN:g1504052
A;Cross-references: EMBL:D87042; PIDN:g1504052; PIDN:g1504052; PIDN:g1504052; PIDN:g1504062; PIDN:g1504062; PIDN:g1504062; PIDN:g1504062; PIDN:g1504062; PIDN:g1504062; PIDN:g1504062; PIDN:g1504062; PIDN:g1504062; PIDN:g1504062; PIDN
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probable calmodulin-domain protein kinase CPK6 [imported] - Arabidopsis thaliana (Species: Arabidopsis thaliana (mouse-ear cress)
C;Bote: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Mar-2001
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Mar-2001
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Mar-2001
C;Date: 02-Keb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Mar-2001
C;Date: 02-Mar-2001
C;Date: 02-Mar-2001
C;Date: 02-Mar-2001
C;Mitch: 0.; Eisen, J.A.; Senito, M.I.; Town, C.D.; Fujii, C.Y., Mature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A64420; MUID:20083487; PMID:10617197
A;Accession: D84520
A;Actus: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-544 <STO>
C;Genetics:
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A;Map position: 2
C;Superfamily: calcium-dependent protein kinase; calmodulin repeat homology; protein k1:
C;Keywords: EF hand
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  65 NVDNQSYYVLGHKTPNIRDLYTLSRKLGQGQFGTTYLCTDIATGVDYACKSISKRKLISK 124
                                                                                                                                                                                                                                                                                                                                                                                        DVVGSPYYVAPEVLLKRYGPEADVWTAGVILYILLSGVPPFWAETQQGIFDAVLKGYIDF 316
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  126 BAVKLIKTILGVVEACHSLGVMRDLKPENFLFDSPKDDAKLKATDFGLSVFYKPGQYLY 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                        KSDPWPTISEAAKDLIYKMLERSPKKRISAHEALCHPWIVDEQAAPDKPLDPAVLSRLKQ 305
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      497 QACVEHGMADVFLEDIIKEVDQNNDGKIDYGEFVEMMQKGNAGVGR-RTMRNSLNISNRD
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                                                                                                                                DVVGSPYYVAPEVLKKCYGPEIDVWSAGVILYILLSGVPPFWAETESGIFRQILQGKLDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEIKSLMDAADIDNSGTIDYGEFLAATLHMNKMEREEILVAAFSDFDKDGSGYITIDELQ
                                                                                         EDYEDVWREIQIMHHLSEHPNVVRIKGTYEDSVFVHIVMEVCEGGELFDRIVSKGHFSER
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66.8%; Score 1731; DB 2; Length 544;
Best Local Similarity 68.3%; Pred. No. 1.2e-57;
Matches 328; Conservative 65; Mismatches 85; Indels
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A; Introns: 252/1; 300/1; 351/1; 389/3; 445/3; 520/3

A; Introns: 252/1; 300/1; 351/1; 389/3; 445/3; 520/3

C; Superfamily: calcium-dependent protein kinase; calmodulin repeat homology; protein kinase

E; 55.355/Domain: protein kinase homology «KIN»

F; 398-430/Domain: calmodulin repeat homology «EF1»

F; 434-466/Domain: calmodulin repeat homology «EF2»

F; 470-502/Domain: calmodulin repeat homology «EF2»

F; 504-555/Domain: calmodulin repeat homology «EF2»
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DAADIDNSGTIDYGEFLAATLHMNKMEREEILVAAFSDFDKDGSGYITIDELQSACTEFG 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             438 DAADIDNNGTIDYIEFIAATLHLNKLEREEHLVAAFSYFDKOGSGYITVDELQQACKEHN 497
                                                                                                                                                                                                                                                                                          REIQIMHHLSEHPNVVRIKGTYEDSVFVHIVMEVCEGGELFDRIVSKGHFSEREAVKLIK 132
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                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     133 TILGVVEACHSLGVMHRDLKPENFLFDSPKDDAKLKATDFGLSVFYKPGQYLYDVVGSPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         253 ISBAAKDLIYKMLERSPKKRISAHEALCHPWIVDEQAAPDKPLDPAVLSRLKQFSQWNKI
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                                                                                                                                                                                             ;;
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Myesidues: 1-556 <BEV>
A;Cross-references: EMBL:AL022604; GSPDB:GN00062; ATSP:F23E12.130
A;Cross-references: EMBL:AL022604; GSPDB:GN00062; ATSP:F23E12.130
A;Experimental source: cultivar Columbia; BAC clone F23E12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 556;
                                                                                                                                   Length 554;
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4.9e-58;
ches 84;
                                                                                                                                   67.3%; Score 1745; DB 1;
ilarity 70.0%; Pred. No. 3.8e-58;
Conservative 57; Mismatches 84;
            F;464-496/Domain: calmodulin repeat homology <EF3>F;498-530/Domain: calmodulin repeat homology <EF4>F;120/Active site: Lys #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
67.2%; Score 1742; DI
Best Local Similarity 68.4%; Pred. No. 4.9e
Matches 329; Conservative 66; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C,Genetics:
A,Gene: CPK5; ATSP:F23E12.130
                                                                                                                                                                   Similarity
                                                                                                                                                                       Best Local Sim
Matches 333;
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Calcium-dependent protein kinase (EC 2.7.1.-) CDPK - pumpkin
NyAlternate names: calcium-dependent calmodulin-independent protein kinase CDPK
(Specias: Cucurbita pepo (pumpkin)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000
C;Accession: T09940
C;Accession: T09940
C;Accession: T09940
C;Accession: T09940
C;Accession: T09940
C;Accession: T09940
C;Accession: T09940
C;Accession: T09940
A;Ritle: Cloning, expression and N-terminal myristoylation of CpCPK1, a calcium-depende
A;Recerace number: 216898; MUID:99178773; PMID:10080688
A;Accession: T09940
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Rocleule type: mRNA
A;Rocleule type: mRNA
A;Rocleule type: mRNA
A;Rocleule type: mRNA
A;Rocleule type: mRNA
A;Cross-references: EMBL:U90262; NID:91899174; PIDN:AAB49984.1; PID:91899175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A, Description: serine/threonine-specific protein kinase activated by direct binding of C; Superfamily: calcium-dependent protein kinase; calmodulin repeat homology; protein kinase; cs, Keywords. APP, calcium binding; EF hand; membrane protein; myristylation; phosphotrar F;108-368/Domain: protein kinase homology «KIN»
F;447-479/Domain: calmodulin repeat homology «EPH»
                                                                                                                                                                                                                                                                                                                                                                                        ABTESGIFRQILQGKLDFKSDPWPTISEAAKDLIYKMLERSPKKRISAHEALCHPWIVDE 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  288 QAAPDKPLDPAVLSRLKQFSQMNKIKKMALRVIABRLSEEBIGGLKELFKMIDTDNSGTI 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PWIVDEQAAPDKPLDPAVLSRLKQFSQMNKIKKMALRVIAERLSEEEIGGLKELFKMIDT 341
                                                                                                           406 PWVQVDGVAPDKPLDSAVLSRMKQFSAMNKFKKMALRVIAESLSEBEIAGLKEMFNMIDA 465
                                                                                                                                                                                      DNSGTITFEELKAGLKRVGSELMESEIKSLMDAADIDNSGTIDYGEFLAATLHNNKMERE 401
                                                                                                                                                                                                                                                                466 DKSGOITFEELKAGLKRVGANLKESEILDLMQAADVDNSGTIDYKEFIAATLHLNKIERE 525
                                                                                                                                                                                                                                                                                                                                               402 EILVAAFSDFDKDGSGYITIDELQSACTEFGLCDTPLDDMIKEIDLDNDGKIDFSEFTAM 461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           72 KPEPPMEPKVRPVMKRVGSAGLRGGSVLQTKTGNFKEYYSLGKKLGQGQFGTTYMCVEKA 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     48 TSANYACKSIPKRKIVCREDYEDVWREIQIMHHLSEHPNVVRIKGTYEDSVFVHIVMEVC 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       132 TGKEYACKSIAKRKLVNEDDVEDVRREIQIMHHLSGHPNVISIKGAYEDAVAVQVVMELC 191
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  252 KTIDFGLSMFFKPGEKFNDVVGSPYYVAPBVLRKRYGPBADVWSAGVIVYILLSGVPPFW 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               348 TFEELKAGLKRVGSELMESEIKSLMDAADIDNSGTIDYGEFLAATLHMNKMEREEILVAA 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        192 AGGELFDRIIQRGHYTERKAAELTRTIVGVLEACHALGVMHRDLKPENFLFVSKEBESLL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       65.9%; Score 1709.5; DB 2; Length 573;
64.8%; Pred. No. 8e-57;
Live 78; Mismatches 79; Indels 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    462 MRKGDGVGRSRTMMKNLNFNIA 483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          586 MOKGSITGGPVKMGLEKSFSIA 607
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Best Local Similarity 64.8%
Matches 321; Conservative
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                                         282
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C.Species: Arabidopsis thaliana (mouse-ear cress)
C.FACCESSION: A49082
R.HATDER, J.F., Binder, B.M.; Sussman, M.R.
Biochemistry, 32, 3282-3290, 1993
A.Title: Calcium and lipid requlation of an Arabidopsis protein kinase expressed in Esch A.FCETENCE number: A49082, WUID:93213795; PMID:7916621
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        286 HEDSLLKTIDFGLSMFFKPDDVFTDVVGSPYYVAPEVLRKRYGPEADVWSAGVIVYILLS 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 102 IVMEVCEGGELFDRIVSKGHFSERBAVKLIKTILGVVEACHSLGVMHRDLKPENFLFDSP 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   162 KDDAKLKATDFGLSVFYKPGQYLYDVVGSPYYVAPEVLKKCYGPEIDVWSAGVILYILLS 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DVVGSPYYVAPEVLKKCYGPEIDVWSAGVILYILLSGVPPFWAETESGIFRQILQGKLDF 245
                                                                                                                   245 DVVGSPYYVAPEVLLKHYGPRADVWTAGVILYILLSGVPPFWAETQQGIFDAVLKGYIDF 304
                                                                                                                                                                                                                           246 KSDPWPTISEAAKDLIYKVIERSPKKRISAHEALCHPWIVDEQAAPDKPLDPAVLSRLKQ 305
                                                                                                                                                                                                                                                                             305 DIDPWPVISDSAKDLIRKMLCSSPSERLTAHEVLRHPWICENGVAPDRALDPAVLSRLKQ 364
                                                                                                                                                                                                                                                                                                                                                                                    306 FSQMNKIKKMALRVIAERLSEEEIGGLKELFKMIDTDNSGTITFEELKAGLKRVGSELME 365
                                                                                                                                                                                                                                                                                                                                                                                                                                  365 FSAMMKLKKWALKVIAESLSREEIAGLRAMFEAMDTDNSGAITFDELKAGLRRYGSTLKD 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     366 SEIKSLMDAADIDNSGTIDYGEFLAATLHMNKMEREEILVAAFSDFDKDGSGYITIDELQ 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               42 LCTEKSTSANYACKSIPKRKLVCREDYEDVWREIQIMHHLSEHPNVVRIKGTYEDSVFVH 101
185 KAAELTKIIVGVVEACHSLGVMHRDLKPENFLLVNKDDDFSLKAIDFGLSVFFVFGQIFK 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      426 SACTEFGLCDTPLDDMIKEIDLDNDGKIDFSEFTAMMRKGD-GVGRSRTMMKNLNFNIAD 484
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65.5%; Pred. No. 2.5e-57;
tive 62; Mismatches 91; Indels 2
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Best Local Similarity 65.55
Matches 329; Conservative
                                                                          186
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A; Description: probably involved in pathogen defense in maize plants
C; Superfamily: calcium-dependent protein kinase; calmodulin repeat homology; protein kinase; C; Keywords: ATP; calcium-binding; EP hand; phosphotransferase; serine/threonine-specific p; 151-411/Domain: protein kinase homology «KIN»
F; 151-411/Domain: protein kinase ATP-binding motif F; 454-486/Domain: calmodulin repeat homology «EFI»
F; 450-522/Domain: calmodulin repeat homology «EFI»
F; 550-522/Domain: calmodulin repeat homology «EFI»
                                                                                                                                                                                                                                                                                             C;Accession: T02784
R;Muxillo, I.; Jaeck, E.; Cordero, M.; San Segundo, B.
Rpmitted to the EMBL Data Library, July 1998
A;Description: A calcium-dependent protein kinase possibly involved in pathogen defense
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ٠<u>,</u>
                                                                                                                                                                                        calcium-dependent protein kinase (EC 2.7.1.-) - maize (strain W64A)
C.Species: Zea mays (maize)
C.Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change 16-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      232
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        120 PSPRPRPQVKRVSSAGLLLGSVLRRKTENLKDKYSLGRRLGQGQFGTTHLCVERATGKEL
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                               CDIPLODMIKEIDLONDGKIDFSEFTAMMRKGDGVGRSRIMMKNLNFNI
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64.5%; Score 1672.5; DB 1;

Best Local Similarity 66.2%; Pred. No. 2e-55;

Matches 318; Conservative 66; Mismatches 83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A,Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-639 «MUR>
A;Residues: references: EMBL:AJ007366; PIDN:CAA07481.1
A;Experimental source: strain W64A; seed
                                                                                                                                                                                                                                                                                                                                                                                                              sis-related PRms gene.
A; Reference number: Z14736
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C;Accession: T05650
R;Bevan, M.; Wedler, H.; Kutzner, M.; Wambutt, R.; Bancroft, I.; Mewes, H.W.; Mayer, K.F
submitted to the Protein Sequence Database, February 1999
A;Reference number: 215420
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                                                                                                                                                                                                                                                                                                                                                                                                                 calcium-dependent protein kinase (EC 2.7.1.-) F20D10.350 - Arabidopsis thaliana N,Alternate names: protein F20D10.350
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 21-Jan-2000
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FSDFDXDGSGYITIDELQSACTEFGLCDTPLDDMIKEIDLDNDGKIDFSEFTAMMRKGDG
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A;Residues: 1-484 <BEV>
A;Cross-references: EMEL:AL035538
A;Experimental source: cultivar Columbia; BAC clone F20D10
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A;Introns: 179/1; 227/1; 278/1; 316/3; 372/3; 447/3
A;Note: F20D10.350
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probable calcium-dependent protein kinase [imported] - Arabidopsis thaliana Cispecies: Arabidopsis thaliana (mouse-ear cress)
C.Species: Arabidopsis thaliana (mouse-ear cress)
C.Accession: H84810
C.Accession: H84810
C.A. K. Kaul, S.; Rounsley, S.D.; Shea, T.F.; Benito, M.I.; Town, C.D.; Fulin, X.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Walaken, S.E.; Fraser, C.M.; Venter, J. Nature 402, 761-768, 1999
A.Reference mumber: A84420; MUID:20083487; PMID:10617197
A.Accession: H84810
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A.Molecule type: DNA
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A;Map position: 2
C;Superfamily: calcium-dependent protein kinase; calmodulin repeat homology; protein kin
C;Keywords: EF hand
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ALIGNMENTS

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Out-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
4-CAT-2001 (Rel. 40, Last annotation update)
AXI OR ATSG04870 OR MUXII.19.
AXI OR ATSG04870 OR MUXII.19.
Bukaryota, Viidiplantae; Streptophyta; Embryophyta; Tracheophyta; Eukaryota, Viidiplantae; Streptophyta; Embryophyta; Rosidae; eurosids II; Erassicales; Brassicaceae; Arabidopsis.
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                                                                                                                                                                                                                                75.0%; Score 1944; DB 1; Length 508;
      Serine/threonine-protein kinase; ATP-binding;
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Transferase; Serine/threonine-prote Calcium-binding; Phosphorylation.

23 29 PROTEIN 40 40 ATP (B BINDING 63 63 ATP (B BINDING 74 BIND 348 359 EF-HAN CA_BIND 420 431 EF-HAN SEQUENCE 508 AA; 57169 MW; AFCE
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Matches 370; Conservative
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                                                                       "Structural analysis of Arabidopsis thaliana chromosome 5. III.
Sequence features of the regions of 1,191,918 bp covered by seventeen
physically assigned P1 clones.";
DNA Res. 4:401-414(1997).
INDIA Res. 4:401-414(1997).
INDIA RES. CALCIUM AS A SECOND MESSENGER.
INVOLVE RECULATION: ACTIVATED BY CALCIUM. AUTOPHOSPHORYLATION MAY
PLAY AN IMPORTANT ROLE IN THE REGULATION OF THE KINASE ACTIVITY.

-!- MISCELLANBOUS: THERE ARE MULTIPLE CDPK ISOFORMS IN MOUSE-EAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     166 LCVEKTIGKEFACKSIAKRKLLIDEDVEDVRREIQIMHHLAGHPNVISIKGAYEDVVAVH 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                102 IVMEVCEGGELFDRIVSKGHFSERBAVKLIKTILGVVEACHSLGVMHRDLKPENFLFDSP 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        226 LVMECCAGGELFDRIIQRGHYTERRAAELTRTIVGVVEACHSLGVMHRDLKPENFLFVSK 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              162 KDDAKLKATDFGLSVFYKPQQYLYDVVGSPYYVAPEVLKKCYGPEIDVWSAGVILYILLS 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       106 BTKPESKPDPPAKPKKPKHMKRVSSAGLRTESVLQRKTENFKEFYSLGRKLGQGQFGTTF 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LCTEKSTSANYACKSIPKRKLVCREDYEDVWREIQIMHHLSEHPNVVRIKGTYEDSVFVH 101
STRAIN-cv. Columbia;
MEDLINE-98162728; PubMed-9501997;
Makamura Y., Sato S., Kaneko T., Kotani H., Asamizu E., Miyajima N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                     -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES. CAMK SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RARET; SM00520; STRC; 1.

RARET; SM00520; STRC; 1.

R PROSITE; PS001019; EFF HAND, 4.

R PROSITE; PS001019; PROTEIN KINASE ATP; 1.

R PROSITE; PS001019; PROTEIN KINASE ATP; 1.

R PROSITE; PS001019; PROTEIN KINASE ATP; 1.

R PROSITE; PS001019; PROTEIN KINASE ATP; 1.

R TARRÉGEASE; SETINE/CHREOTINE-PROTEIN KINASE; ATP-binding; Calcium-binding; Phosphorylatron; Multigene family.

R MIDING 150 109 PROTEIN KINASE;

I DOMAIN 150 179 ATP (BY SIMILARITY).

R MIDING 179 179 ATP (BY SIMILARITY).

I ACT SITE 274 475 BF-HAND 1 (POTENTIAL).

I CA BIND 530 511 EF-HAND 2 (POTENTIAL).

I CA BIND 530 547 EF-HAND 4 (POTENTIAL).

I CA BIND 570 581 EF-HAND 4 (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            66.5%; Score 1724; DB 1; Length 610; 65.5%; Pred. No. 2.2e-79;
                                                                                                                                                                                                                                                                                                                               -!- SIMILARITY: CONTAINS 4 EF-HAND CALCIUM-BINDING DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      91; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PIR: A49082, A49082.
HSSP; P02588; 1PON.
HSSP; P02588; 1PON.
InterPro; IPR0020449; EF-hand.
InterPro; IPR0002049; Ser_thr_pkinase.
InterPro; IPR002290; Ser_thr_pkinase.
Pfam; PP00059; Pkinase; 1.
ProDom; PD000001; Elw pkinase; 1.
ProDom; PD000001; Er-hand; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AB008271; BAB08991.1; -.
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PRT;
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Best Local Similarity 63.94
Matches 304; Conservative
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                                                                                            89
107
202
404
440
476
510
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P53683;
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DOMAIN
CA BIND
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=CV. Arborio, TISSUE=Coleoptile;

X MEDLINE=9528432; PubMed=7766885;
Breviatio D., Morello L., Giani S.,
Breviatio D., Morello L., Giani S.,
Calcium-dependent protein kinases.";
Calcium-dependent protein kinases.";
Plant Mol. Biol. 27:953-967(1995).
C.:- FUNCTION: MAY PLAY A.ROLE IN SIGNAL TRANSDUCTION PATHWAYS THAT
COLUMNOLYBE REGILATION: ACTIVATED BY CALCIUM (BY SIMILARITY).
C.:- BNZYME REGILATION: ACTIVATED BY CALCIUM (BY SIMILARITY).
C.:- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
C.:- SIMILARITY: CONTAINS 4 EF-HAND CALCIUM-BINDING DOWAINS. THREE OF THEM SEEM TO BE NON FUNCTIONAL.
                                                              405
HEDSLLKTIDFGLSMFFKPDDVFTDVVGSPYYVAPEVLRKRYGPEADVWSAGVIVYILLS 345
                                                                                              PWIVDEQAAPDKPLDPAVLSRLKQFSQMNKIKKMALRVIAERLSEBEIGGLKELFKMIDT 341
                                                                                                                 DNSGTITFEELKAGLKRVGSELMESEIKSLMDAADIDNSGTIDYGEFLAATLHMNKMERE 401
                                                                                                                                                                                            525
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1-OCT-2096 (Rel. 34, Last sequence update)
16-OCT-2001 (Rel. 40, Last anotation update)
Calcium-dependent protein kinase, isoform 11 (EC 2.7.1.-) (CDPK 11)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Viridiplantae, Streptophyta, Embryophyta, Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopaida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                DKSG01TFEELKAGLKRVGANLKESEILDLMQAADVDNSGTIDYKEFIAATLHLNKIERE
                                                                                                                                                                                                                                                BILVAARSDFDKDGSGYITIDELQSACTEFGLCDTPLDDMIKEIDLDNDGKIDFSEFTAM
                                                GVPPFWAETESGIFROILOGKLDFKSDPWPTISEAAKDLIYKMLERSPKKRISAHEALCH
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INCETPO; IPRO02019; Euk_pkinase.
INCETPO; IPRO00219; Euk_pkinase.
Pfam; PF00036; efhand; 4—
Pfam; PF000016; Ekhand; 4.
PF0Dom; PD00001; Euk_pkinase; 1.
PF0Dom; PD00001; Euk_pkinase; 1.
PF0Dom; PD00001; Euk_pkinase; 1.
PF0Dom; PD00001; Erk_phind; 2.
SMART; SM00220; S_TKC; 1.
                                                                                                                                                                                                                                                                                              462 MRKGDGVGRSRTMMKNLNFNIA 483
                                                                                                                                                                                                                                                                                                                   EMBL; X81393; CAA57156.1; -.
HSSP; Q63450; 1A06.
                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CPK11.
Oryza sativa (Rice)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=4530;
                                                                                                                                                                                                                                                                                                                                                                                                               ORYSA
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CDP3 ORY P53684; RESULT 3 CDP3 ORYSA

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STRAIN=CV. Arborio; TISSUE=Coleoptile;
MEDLINE=95284352; PubMed=7766885;
Breviario D., Morello L., Giani S.;
"Molecular cloning of two novel rice cDNA sequences encoding putative calcium-dependent protein kinases.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          243
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    303
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                       (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       64 SINVLGRKTADLREHYIIGRKLGQAQFGTTYLCTEINTGCEYACKTIPKRKLITKEDVED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   71 VWREIQIMHHLSEHPNVVRIKGTYEDSVFVHIVMEVCEGGELFDRIVSKGHFSEREAVKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                124 VRREIQIMHHLSGHKNVVAIKDVEDGQAVHIVMELCAGGELFDRIQEKGHYSERKAAEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             131 IKTILGVVEACHSLGVMHRDLKPENFLFDSPKDDAKLKATDFGLSVFYKPGQYLYDVVGS
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01-0CT-1996 (Rel. 34, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Calcium-dependent protein kinase, isoform 2 (EC 2.7.1.-) (CDPK 2)
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PROSITE; PS00016; EF HAND; 1.
PROSITE; PS00119; PROTEIN KINASE_ST; 1.
PROSITE; PS0011; PROTEIN KINASE_DCM; 1.
Transferase; Serine/threonine-protein kinase; ATP-binding; Calcium-binding; Phosphorylation; Multigene family.
DOMAIN
NP BIND
81 89 ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
ACT SITE 202 202 BY SIMILARITY.
DOMAIN 393 404 ANDESTRAL CALLIUM SITE 1 (POT MOMENTAL SITE 202 ANDESTRAL CALLIUM SITE 1 (POT MOMENTAL SITE 202 ANDESTRAL CALLIUM SITE 1 (POT MOMENTAL SITE 202 ANDESTRAL CALLIUM SITE 1 (POT MOMENTAL SITE 202 ANDESTRAL CALLIUM SITE 1 (POT MOMENTAL SITE 202 ANDESTRAL CALLIUM SITE 1 (POT MOMENTAL SITE 202 ANDESTRAL CALLIUM SITE 1 (POT MOMENTAL SITE 202 ANDESTRAL CALLIUM SITE 1 (POT MOMENTAL SITE 202 ANDESTRAL CALLIUM SITE 1 (POT MOMENTAL SITE 202 ANDESTRAL CALLIUM SITE 1 (POT MOMENTAL SITE 202 ANDESTRAL CALLIUM SITE 1 (POT MOMENTAL SITE 202 ANDESTRAL CALLIUM SITE 1 (POT MOMENTAL SITE 202 ANDESTRAL CALLIUM SITE 1 (POT MOMENTAL SITE 202 ANDESTRAL CALLIUM SITE 1 (POT MOMENTAL SITE 202 ANDESTRAL CALLIUM SITE 1 (POT MOMENTAL SITE 202 ANDESTRAL CALLIUM SITE 1 (POT MOMENTAL SITE 202 ANDESTRAL CALLIUM SITE 1 (POT MOMENTAL SITE 202 ANDESTRAL CALLIUM SITE 1 (POT MOMENTAL SITE 202 ANDESTRAL CALLIUM SITE 1 (POT MOMENTAL SITE 202 ANDESTRAL CALLIUM SITE 1 (POT MOMENTAL SITE 202 ANDESTRAL CALLIUM SITE 2 (POT MOMENTAL SITE 202 ANDESTRAL CALLIUM SITE 2 (POT MOMENTAL SITE 202 ANDESTRAL CALLIUM SITE 2 (POT MOMENTAL SITE 202 ANDESTRAL CALLIUM SITE 2 (POT MOMENTAL SITE 202 ANDESTRAL CALLIUM SITE 2 (POT MOMENTAL SITE 202 ANDESTRAL CALLIUM SITE 2 (POT MOMENTAL SITE 202 ANDESTRAL CALLIUM SITE 2 (POT MOMENTAL SITE 202 ANDESTRAL CALLIUM SITE 2 (POT MOMENTAL SITE 202 ANDESTRAL CALLIUM SITE 2 (POT MOMENTAL SITE 202 ANDESTRAL CALLIUM SITE 2 (POT MOMENTAL SITE 202 ANDESTRAL CALLIUM SITE 2 (POT MOMENTAL SITE 202 ANDESTRAL CALLIUM SITE 2 (POT MOMENTAL SITE 202 ANDESTRAL CALLIUM SITE 2 (POT MOMENTAL SITE 202 ANDESTRAL SITE 202 ANDESTRAL SITE 202 ANDESTRAL SITE 202 ANDESTRAL SITE 202 ANDESTRAL SITE 202 ANDESTRAL SITE 202 ANDESTRAL SITE 20
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ANCESTRAL CALCIUM SITE 1 (E
ANCESTRAL CALCIUM SITE 2 (E
ANCESTRAL CALCIUM SITE 2 (E
EF-HAND 4 (POTENTIAL)
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390
4426
462
797
                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                      MaizeDB; 56895;
                                                                                CDP2 MAIZE P49101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
NP_BIND
BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CA_BIND
CA_BIND
CA_BIND
                                                                RESULT 5
CDP2_MAIZE
ID _CDP2_M
                       424
                                        482
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                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KOFSOMNKIKKWALRVIAERLSEEEIGGLKELFKMIDTDNSGTITFEELKAGLKRVGSEL 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  184 LYDVVGSPYYVAPEVLKKCYGPEIDVWSAGVILYILLSGVPPFWAETESGIFRQILQGKL 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       364 MESEIKSLMDAADIDNSGTIDYGEFLAATLHMNKMEREEILVAAFSDFDKDGSGYITIDE 423
                                                                                                                                                                                                                                                                                                                                                                                                                          64 CREDYEDVWREIQIMHHLSEHPNVVRIKGTYEDSVFVHIVMEVCEGGELFDRIVSKGHFS 123
                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                               4 KPNPRRPSNTVLPYQTPRLRDHYLLGKKLGQGQFGTTYLCTEKSTSANYACKSIPKRKLV 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 124 EREAVKLIKTILGVVEACHSLGVMHRDLKPENFLFDSPKDDAKLKATDFGLSVFYKPGQY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           244 DFKSDPWPTISEAAKDLIYKMLERSPKKRISAHEALCHPWIVDEQAAPDKPLDPAVLSRL
Plant Mol. Biol. 27:953-967(1995).
-!- FUNCTION: MAY PLAY A ROLE IN SIGNAL TRANSDUCTION PATHWAYS THAT INVOLVE CALCIUM AS A SECOND MESSENGER.
-!- ENZYME REGULATION: ACTIVATED BY CALCIUM (BY SIMILARITY).
-!- MISCELLANBOOUS: THERE ARE MULTIPLE CDPK ISOFORMS IN RICE.
-!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CAMK SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                               .
9
                                                                                                                                                           Length 533;
                                                         -!- SIMILARITY: CONTAINS 4 BF-HAND CALCIUM-BINDING DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                              98; Indels
                                                                                                                                                                                                                                                                                                                   BY SIMILARITY.

EF-HAND 1 (POTENTIAL).

EF-HAND 2 (POTENTIAL).

EF-HAND 3 (POTENTIAL).

EF-HAND 4 (POTENTIAL).

4, DOBC570ABD289E28 CRC64;
                                                                                                                                                                                                                                                                                          PROTEIN KINASE.
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                              57.2%; Score 1482; DB 1; 61.3%; Pred. No. 2.2e-67;
                                                                                                                                                                                                                                                                                                                                                                                     61.3%; Pred No --
                                                                                                                                                                                                                                                                                                                                                              59522 MW;
                                                                                                                                            EMBL; X81394; CAA57157.1; -. HSSP; Q63450; 1A06.
                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                            114
209
398
434
470
470
505
533 AA;
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Best Local Simi
Matches 284;
                                                                                                                                                                                                                                                                                           DOMAIN
NP BIND
BINDING
ACT SITE
CA BIND
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CA BIND
CA BIND
CA BIND
CA BIND
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Zea mays (Maize).
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
OF THE KINASE ACTIVITY (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE SER/THR PAMILY OF PROTEIN KINASES.
COMM. SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R Interpro; IPR000719; Euk_pkinase.
R Interpro; IPR000719; Euk_pkinase.
R Interpro; IPR000719; Euk_pkinase.
R Interpro; IPR000719; Euk_pkinase.
R Interpro; IPR000290; Ser thr_pkinase.
R Pfam; PF000069; pkinase; 1.
R PF000m; PE000001; EPk_pkinase; 1.
R PF000m; PE000012; EFh 4.
R SMART; SM00024; EFh 4.
R SMART; SM00020; EFh 4.
R PR05ITE; PS00107; PROTEIN_KINASE_AIP; 1.
R PR05ITE; PS00107; PROTEIN_KINASE_AIP; 1.
R PR05ITE; PS00109; PROTEIN_KINASE_EOM; 1.
R PR05ITE; PS00109; PROTEIN_KINASE_EOM; 1.
R PR05ITE; PS00109; PR0FINI KINASE_EOM; 1.
R PR05ITE; PS00109; PR0FINI KINASE_EOM; 1.
R PR05ITE; PS00109; PR0FINI KINASE_EOM; 1.
R PR05ITE; PS00109; PR0FINI KINASE.
I DOWAIN
I DOWAIN G 5323 PR0FINI KINASE.
I NP_BIND 71 79 AIP (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- SIMILARITY: CONTAINS 4 EF-HAND CALCIUM-BINDING DOMAINS
                                                                                                                                                                                                                                                                                                                                  01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
16-02-2001 (Rel. 40, Last amnotation update)
Calcium-dependent protein kinase 2 (EC 2.7.1.-) (CDPK 2)
                                                                                      LOSACTEFGLCDT-PLDDMIKEIDLDNDGKIDFSEFTAMMRKG 465
                                                                                                                      (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROTEIN KINASE.
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
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EF-HAND 1 (POT
EF-HAND 2 (POT
EF-HAND 3 (POT
EF-HAND 4 (POT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Merrit; TISSUE=Root tip;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Spermitophyta, Magnoliophyta; Lip
Panicoideae, Andropogoneae, Zea.
NCBI_TaxID=4577;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; U28376; AAA69507.1; -.
HSSP; Q63450; 1A06.
                                                                                                                                                                                                                                                                                 STANDARD;
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RESULT 7
CDPK DAUCA
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                                                                                                    186
                            Gaps
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                                          7 PRRPSNIVLPYQIPRLRDHYLLGKKLGQGQFGTTYLCTEKSTSANYACKSIPKRKLVCRE 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                              THAT
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                                                                                                                                                                                                                                                                                                                                                     Oryza sativa (Rice).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Nagnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaa; Oryza.
                                                                                DYEDVWREIQIMHHLSEHPNVVRIKGTYEDSVFVHIVMEVCEGGELFDRIVSKGHFSERE
                                                                                                                                 187 VVGSPYYVAPEVLKKCYGPEIDVWSAGVILYILLSGVPPFWAETESGIFRQILQGKLDFK
                                                                                                                                                              SDPWPTISEAAKDLIYKMLERSPKKRISAHEALCHPWIVDEQAAPDKPLDPAVLSRLKQF
                                                                                                                                                                       307 SOMNKIKKMALRVIAERLSEEFIGGLKELFKMIDTDNSGTITFEELKAGLKRVGSELMES
                                                                                                                                                                                                  AVKLIKTILGVVEACHSLGVMHRDLKPENFLFDSPKDDAKLKATDFGLSVFYKPGQYLYD
                                                                                                                                                                                                                       EIKSLMDAADIDNSGTIDYGEFLAATLHMNKMEREEILVAAFSDFDKDGSGYITIDELQS
                                                                                                                                                                                                                                                                                                                    01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
16-OCT-2001 (Rel. 40, Last amnotation update)
Calcium-dependent protein kinase, isoform 1 (EC 2.7.1.-) (CDPK 1)
                            1,
              56.3%; Score 1460.5; DB 1; Length 60.0%; Pred. No. 2.5e-66; ive 78; Mismatches 105; Indels
58081 MW; 235A61630C0AC336 CRC64;
                                                                                                                                                                                                                                                     427 ACTEFGLCDT-PLDDMIKEIDLDNDGKIDFSEFTAMMRKG 465
                                                                                                                                                                                                                                                             ALIEHEMGDTSTIREIISEVDTDNDGRINYEEFCAMMRGG 505
                                                                                                                                                                                                                                                                                                      534 AA
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                             Conservative
                                                                                                                                                                                                                                                                                                      STANDARD;
AA;
                      Similarity
513
                                                                                                                                                                                                                                                                                                                    01-OCT-1996 (
01-OCT-1996 (
16-OCT-2001 (
                             Matches 276;
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              Query Match
Best Local S
SEQUENCE
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CDP1_ORYSA
ID _CDP1_ORY:
AC P53682;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BY SIMILARITY.
ANCESTRAL CALCIUM SITE 1 (FOTENTIAL)
ANCESTRAL CALCIUM SITE 2 (FOTENTIAL)
ANCESTRAL CALCIUM SITE 3 (FOTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4
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R SYART; SMO0054; EFh; 2.

SYART; SMO0059; EF FAND; 1.

R PROSITE; PSO0109; PROTEIN KINASE ATP; 1.

R PROSITE; PSO0109; PROTEIN KINASE DOM; 1.

R PROSITE; PSO0109; PROTEIN KINASE DOM; 1.

W Transferase; Serine/threonine-protein kinase; ATP-binding; ACCIOUM-binding; PROTEIN KINASE DOM; 1.

R TRANSferase; Serine/threonine-protein kinase; ATP-binding; ACCIOUM-binding; PROTEIN KINASE DOM; 1.

R TRANSFERASE; SERINE/THREONING; PROTEIN KINASE, PROTEIN KINASE, ATP-BINDING; PROTEIN KINASE, ATP-BINDING; PROTEIN KINASE, ATP-BINDING; PROTEIN KINASE, ATP-BINDING; PROTEIN KINASE, ATP-BINDING; PROTEIN KINASE, ATP-BINDING; PROTEIN KINASE, ATP-BINDING; PROTEIN KINASE, ATP-BINDING; PROTEIN KINASE, ATP-BINDING; PROTEIN KINASE, ATP-BINDING; PROTEIN KINASE, ATP-BINDING; PROTEIN KINASE, ATP-BINDING; PROMENING; PROMENING; PROMENING; PROMENING; PROMENING; PROMENING; PROMENING; PROMENING; PROMENING; PROMENING; PROMENING; PROMENING; PROMENING; PROMENING; PROMENING; PROMENING; PROMENING; PROMENING; PROMENING; PROMENING; PROMENING; PROMENING; PROMENING; PROMENING; PROMENING; PROMENING; PROMENING; PROMENING; PROMENING; PROMENING; PROMENING; PROMENING; PROMENING; PROMENING; PROMENING; PROMENING; PROMENING; PROMENING; PROMENING; PROMENING; PROMENING; PROMENING; PROMENING; PROMENING; PROMENING; PROMENING; PROMENING; PROMENING; PROMENING; PROMENING; PROMENING; PROMENING; PROMENING; PROMENING; PROMENING; PROMENING; PROMENING; PROMENING; PROMENING; PROMENING; PROMENING; PROMENING; PROMENING; PROMENING; PROMENING; PROMENING; PROMENING; PROMENING; PROMENING; PROMENING; PROMENING; PROMENING; PROMENING; PROMENING; PROMENING; PROMENING; PROMENING; PROMENING; PROMENING; PROMENING; PROMENING; PROMENING; PROMENING; PROMENING; PROMENING; PROMENING; PROMENING; PROMENING; PROMENING; PROMENING; PROMENING; PROMENING; PROMENING; PROMENING; PROMENING; PROMENING; PROMENING; PROMENING; PROMENING; PROMENING; PROMENING; PROMENING; PROMENING; PROMENING; PROMENING; PROMENING; PROMENING; PROMENING; PROMENING; PROMENING; PROMENING; PROME
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EDTFLEEMILEVDQNNDGQIDYAEFVTWMQSNNFGLG-WQTVESSLNVALREA
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                                                                                                                                                                                                                                                                             EMBL, D13436; BAA02698.1; -...
HSSP, P02593; 1CDM.
IncerPro; IPR002048; EF-hand.
IncerPro; IPR000719; EUk pkinase.
IncerPro; IPR00230; Ser_hr pkinase.
Pfam; PP00003; efhand; 4
Pfam; PP00003; pkinase; 1.
ProDom; PD000001; Euk pkinase; 1.
ProDom; PD0000012; EF-hand; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EF-HAND 4
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Best Local Similarity 59.2'
Matches 280; Conservative
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116 IVSKGHFSEREAVKLIKTILGVVEACHSLGVWHRDLKPENFLFDSPKDDAKLKATDFGLS 175

171 IIAQGHYSERAAATICRQİVNVVHVCHFMGVMHRDLKPENFLLSSKDKDAMLKATDFGLS

SIPKRKLVCREDYEDVWREIQIMHLSEHPNVVRIKGTYEDSVFVHIVMEVCEGGELFDR

51 QTGPSLKPRQVHRPESNTILGKPFEDIRGKYTLGKELGRGQFGCVYQCTENSSGQLYACK 110

RQILQGKLDFKSDPWPTISEAAKDLIYKMLERSPKKRISAHEALCHPWIVDEQAAPDKPL 295

VEYKPGQYLYDVVGSPYYVAPEVLKKCYGPEIDVWSAGVILYILLSGVPPFWAETESGIF 235

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                                                                                                                                                                                                                                                                                                                                                                  calcium/dependent protein Kinase: homology to calcium/dependent protein Kinases homology to calcium/calmodulin-dependent protein kinases and to calmodulin."; plant Mol. Biol. 17:581-590(1991).

-!- FUNCTION: MAY PLAY A ROLE IN SIGNAL TRANSDUCTION PATHWAYS THAT INVOLVE CALCIUM AS A SECOND MESSENGER.

-!- FUXTME REGULARION: ACTIVATED BY CALCIUM. AUTOPHOSPHORYLATION MAY PLAY AN IMPORTANT ROLE IN THE REGULATION OF THE KINASE ACTIVITY.

-!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
   01-DEC-1992 (Rel. 24, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last annotation update)
Calcium-dependent protein kinase (EC 2.7.1.-) (CDPK).
Daucus carota (Carrot).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids II; Apiales; Apiaceae; Daucus.
NCBI_TaxID=4039;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1; Length 532;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R HSSP; 063450; 1A66.

R HSSP; 063450; 1A66.

R HSSP; 063450; 1A66.

R InterPro; IPR002048; EP-hand.

R InterPro; IPR00219; Buk pkinase.

R InterPro; IPR002036; efhand; 4.

R Pfan, PR000036; efhand; 4.

R ProDom; PD000012; EP-hand; 2.

R SMART; SM00050; EPH; 4.

R SMART; SM00050; EPH; 4.

R PROSITE; PS00108; EPH; 4.

R PROSITE; PS00108; PROTEIN KINASE AIP; 1.

R PROSITE; PS00108; PROTEIN KINASE DM; 1.

R PROSITE; PS00108; PROTEIN KINASE DM; 1.

R PROSITE; PS00108; PROTEIN KINASE DM; 1.

R PROSITE; PS00109; PROTEIN KINASE DM; 1.

R PROSITE; PS00109; PROTEIN KINASE DM; 1.

R PROSITE; PS00109; PROTEIN KINASE DM; 1.

R PROSITE; PS00109; PROTEIN KINASE DM; 1.
                                                                                                                                                                                                                                                                                    [2]

REQUENCE OF 108-532 FROM N.A.

MEDLINE=92003674; PubMed=1912486;

Suen K.-L., Choi J.H.;

"Isolation and sequence analysis of a CDNA clone for a carrot "Isolation and sequence homology to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CAMK SUBFAMILY.
-!- SIMILARITY: CONTAINS 4 EF-HAND CALCIUM-BINDING DOMAINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         55.2%; Score 1432.5; DB 1; Length
59.1%; Pred. No. 6.5e-65;
ive 76; Mismatches 107; Indels
                                                                                                                                                                                                                                             Choi J.H.;
Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     F03E6F036A0AE348 CRC64;
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ATP (BY SIMILARITY).
BY SIMILALITY.
EF-HAND 1 (POTENTIAL).
EF-HAND 2 (POTENTIAL).
EF-HAND 3 (POTENTIAL).
EF-HAND 4 (POTENTIAL).
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 STANDARD;
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532 AA;
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 CDPK DAUCA
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DPAVLSRLKQFSQMNKIKKMALRVIAERLSEERIGGLKELFKMIDTDNSGTITFEELKAG 355
                                    LKRVGSELMESEIKSLMDAADIDNSGTIDYGEFLAATLHWNKWEREEILVAAFSDFDKDG 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots;
Asteridae, euasterids II; Apiales, Apiaceae, Daucus.
VCBI_TaxID=4039;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-CCT-1996 (Rel. 34, Created)
01-CCT-1996 (Rel. 34, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
CDPK-related protein kinase (EC 2.7.1.-) (PK421).
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HSSP; Q6450; 1A66.
InterPro; IPR002048; EF-hand.
InterPro; IPR002049; EW pkinase.
InterPro; IPR00209; Ser thr pkinase.
Pfam: PF00069; pkinase; 1.
ProDon; PD000001; Euk_pkinase; 1.
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Matches 278; Conservative

Similarity

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SEQUENCE FROM N.A.
TISSUE=Myocardium;
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                                                                                 3 X 7 AA TANDEM REPEATS OF S-[LI]-P-X-X-D-X.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           :|: || || || ::::| | | | | :
507 RRMDFEEFCAAALSVHQLBALDRWEQHARCAYDLFEKDGNRAIMIBELAS---ELGLGPS 563
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              202 CYGPEIDVWSAGVILYILLSGVPPFWAETESGIFRQILQGKLDFKSDPWPTISEAAKDLI 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 328 SYSTEADVWSIGVISYILLCGSRPFWARTESGIFRAVLKANLSFDEPPWPSVSSEAKDFV 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      262 YKMLERSPKKRISAHEALCHPWIVDEQAAPDKPLDPAVLSRLKQFSQMNKIKKMALRVIA 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          322 ERLSEEBIGGLKELFKMIDTDNSGTITFEELKAGLKRVGSELM-ESEIKSLMDAADIDNS 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EHPNVVRIKGTYEDSVFVHIVMEVCEGGELFDRIVSK-GHFSEREAVKLIKTILGVVEAC 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HSLGVMHRDLKPENFLFDSPKDDAKLKATDFGLSVFYKPGQYLYDVVGSPYYVAPEVLKK 201
                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi<u>i.</u>
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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(POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                               32.9%; Score 854; DB 1; Length 602; 41.2%; Pred. No. 5.1e-36; ive 90; Mismatches 155; Indels
                                                                  Transferase; Serine/threonine-protein kinase; ATP-binding; Repeat.

DOMAIN 20 40 3 X 7 AA TANDEM REPEATS OF S-
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ATP (BY SIMILARITY).

ATP (BY SIMILARITY).

BY SIMILARITY.

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SMART; SM00220; S_TKC; 1.
PROSTE; PS00100; PROTEIN KINASE ATP; 1.
PROSITE; PS00100; PROTEIN_KINASE_ST; 1.
PROSITE; PSS0011; PROTEIN_KINASE_DOM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          437 -PLDDMIKEIDLDNDGKIDFSEFTAMM 462
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Matches 184; Conservative
                                                                                                                                                                                                                                                                                                                                              602 AA;
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MEDILESSES, 900014141, pubMed=10189359, MARIONESSES, C. Karcesskip P., MEDILESSES, 2005161410, MARIONESSES, MARIONESSES, MARIONESSES, MARIONESSES, MARIONESSES, MARIONESSES, MARIONESSES, MARIONESSES, MARIONESSES, MARIONESSES, MARIONESSES, MARIONESSES, MARIONESSES, MARIONESSES, MARIONESSES, MARIONESSES, MARIONESSES, MARIONESSES, MARIONESSES, MARIONESSES, MARIONESSES, MARIONESSES, MARIONESSES, MARIONESSES, MARIONESSES, MARIONESSES, MARIONESSES, MARIONESSES, MARIONESSES, MARIONESSES, MARIONESSES, MARIONESSES, MARIONESSES, MARIONESSES, MARIONESSES, MARIONESSES, MARIONESSES, MARIONESSES, MARIONESSES, MARIONESSES, MARIONESSES, MARIONESSES, MARIONESSES, MARIONESSES, MARIONESSES, MARIONESSES, MARIONESSES, MARIONESSES, MARIONESSES, MARIONESSES, MARIONESSES, MARIONESSES, MARIONESSES, MARIONESSES, MARIONESSES, MARIONESSES, MARIONESSES, MARIONESSES, MARIONESSES, MARIONESSES, MARIONESSES, MARIONESSES, MARIONESSES, MARIONESSES, MARIONESSES, MARIONESSES, MARIONESSES, MARIONESSES, MARIONESSES, MARIONESSES, MARIONESSES, MARIONESSES, MARIONESSES, MARIONESSES, MARIONESSES, MARIONESSES, MARIONESSES, MARIONESSES, MARIONESSES, MARIONESSES, MARIONESSES, MARIONESSES, MARIONESSES, MARIONESSES, MARIONESSES, MARIONESSES, MARIONESSES, MARIONESSES, MARIONESSES, MARIONESSES, MARIONESSES, MARIONESSES, MARIONESSES, MARIONESSES, MARIONESSES, MARIONESSES, MARIONESSES, MARIONESSES, MARIONESSES, MARIONESSES, MARIONESSES, MARIONESSES, MARIONESSES, MARIONESSES, MARIONESSES, MARIONESSES, MARIONESSES, MARIONESSES, MARIONESSES, MARIONESSES, MARIONESSES, MARIONESSES, MARIONESSES, MARIONESSES, MARIONESSES, MARIONESSES, MARIONESSES, MARIONESSES, MARIONESSES, MARIONESSES, MARIONESSES, MARIONESSES, MARIONESSES, MARIONESSES, MARIONESSES, MARIONESSES, MARIONESSES, MARIONESSES, MARIONESSES, MARIONESSES, MARIONESSES, MARIONESSES, MARIONESSES, MARIONESSES, MARIONESSES, MARIONESSES, MARIONESSES, MARIONESSES, MARIONESSES, MARIONESSES, MARIONESSES, MARIONESSES, MARIONESSES, MARIONESSES, MARIONESSES, MARIONESSES, MARIONESSES, MARIONESSES, MARIONESSES, MARIONESSES, M
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118
309
374 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                         Matches 124;
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CONFLICT
CONFLICT
SEQUENCE
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KCC1_HUMAN
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                                                                                                                                                                                                                        199
                                                                                        258
                                                                                                                                                                DLIYKMLERSPKKRISAHEALCHPWIVDEQAAPDKPLDPAVLSRLKQFSQMNKIKKMALR 318
                                                                                                                                                                              319 VIAERLSEEEIGGLKELFKMID-----TDNSG-TITFEELKA---GLKRVGSELMESEIK 369
                                 140
                                                       126
                                                                                                                                                                                                                                                                                                                                                                                                                      Rattus norvegicus (Rat).
Bukaryota, Metazoa, Chordata, Ćraniata, Vertebrata, Buteleostomi;
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              calcium/calmodulin
 9 RFTDEYQLFEELGKGAFSVVRRCMKIPTGQGYAAKIINTKKLSAR-DHQKLEREARIC-R
                                              LSEHPNVVRIKGTYEDSVFVHIVMEVCEGGELFDRIVSKGHFSEREAVKLIKTILGVVEA
                                                                            CHSLGVMHRDLKPENFLFDSPKDDAKLKATDFGLSVFYKPGQYL-YDVVGSPYYVAPEVL
                                                                                                                       KK-CYGPEIDVWSAGVILYILLSGVPPFWAETESGIFRQILQGKLDFKSDPWPTISEAAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. (37 KDA ISOPORM).
MEDLINE=94075341; PubMed=8253780;
Picciotto M.R., Czernik A.J., Nairn A.C.;
"Calcioun/calmodulin-dependent protein kinase I. cDNA cloning and identification of autophosphorylation site.";
J. Biol. Chem. 268:26512-26521(1993).
                                                                                                                                                                                                                                                                                                                                                                                     type I (EC 2.7.1.123)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Goldberg J., Nairn A.C., Kuriyan J.;

"Structural basis for the autoinhibition of

"Structural basis for the autoinhibition of

calcium/calmodulin-dependent protein kinase I.";

Cell 84:875-887(1996)

-!- FUNCTION: PHOSPHORYLATES SYNAPSIN I.

-!- CATALYTIC ACTIVITY: ATP + protein = ADP + O-phosphoprotein.

-!- ENZYME REGULATION: ACTIVATED BY CA++/CALMODULIN. MUST BE

PHOSPHORYLATED TO BE MAXIMALLY ACTIVE.

-!- SUBUNIT: MONOMER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF SHORT FORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    B., Weaver T.E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. (42 KDA ISOFORM).
STRAIN=Sprague-Dawley, TISSUE-Lung;
MEDLINE=95035115; PubMed=7948038;
Cho F.S., Phillips K.S., Bogucki B.; Weaver T.E
"Characterization of a rat cDNA clone encoding
dependent protein kinase I.";
Biochim. Biophys. Acta 1224:156-160(1994).
                                                                                                                                                                                                                                                                                                                                           063450, 063084;
15-UUL-1998 (Rel. 36, Last sequence update)
15-UUL-1998 (Rel. 36, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Calcium/calmodulin-dependent protein kinase ty
(CAM kinase I)
                                                                                                                                                                                                                                                                                                                                 374 AA
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                                                                                                                                                                                                                                                                             361 -----1NNGDFEAYT 370
                                                                                                                                                                                                                                                       370 SLMDAADIDNSGTIDYGEFLAAT 392
                                                                                                                                                                                                                                                                                                                                   STANDARD;
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                                                                                                                                                                                                                                                                                                                                    KCC1 RAT
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R PDB; 1A06; 08-ARR-98

R InterPro; 1PR000239; Ser_thr_pkinase.

R Pfam; PF00069; pkinase; 1.

R Pfam; PF00069; pkinase; 1.

R Pfam; PF000601; Euk_pkinase; 1.

R PADDM; PD000001; PR0TEIN KINASE_ATP; 1.

R PROSITE; PS00100; PROTEIN KINASE_ATP; 1.

R PROSITE; PS00100; PROTEIN KINASE_DOW; 1.

R PROSITE; PS00100; PROTEIN KINASE_DOW; 1.

R PROSITE; PS00100; PROTEIN KINASE_DOW; 1.

R PROSITE; PS00100; PROTEIN KINASE_DOW; 1.

R PROSITE; PS00100; PROTEIN KINASE_DOW; 1.

R PROSITE; PS00100; PROTEIN KINASE_DOW; 1.

R PROSITE; PS00100; PROTEIN KINASE_DOW; 1.

R PROSITE; PS00100; PROTEIN KINASE_DOW; 1.

R PROSITE; PS00100; PROTEIN KINASE_DOW; 1.

R PROSITE; PS00100; PROTEIN KINASE_DOW; 1.

R PROSITE; PS00100; PROTEIN KINASE_DOW; 1.

R PROPERS 32 3 4 ATP (BY SIMILARITY).

R PROPERS 177 177 PHOSPHOYLATION (AUTO-).

R PAPPPSSRAMD -> HQFGGTGTDS (IN 37 KDA FORDERS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its mose by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      78 MHHLSEHPNVVRIKGTYEDSVFVHIVMEVCEGGELFDRIVSKGHFSEREAVKLIKTILGV 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               138 VEACHSLGVMHRDLKPENFLFDSPKDDAKLKATDFGLSVFYKPGQYLYDVVGSPYYVAPE 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                129 VKYLHDLGIVHRDLKPENLLYYSLDEDSKIMISDFGLSKMEDPGSVLSTACGTPGYVAPE 188
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       249 AKDFIRHLMEKDPEKRFTCEQALQHPWIAGDTAL-DKNIHQSVSEQIKKNFAKSKWKQ 305
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
16-CUT-1998 (Rel. 40, Last sequence update)
Calcium/calmodulin-dependent protein kinase type I (EC 2.7.1.123)
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A -> R (IN REF. 1).
A -> R (IN REF. 1).
; 37889B3DEF033AB2 CRC64;
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41.6%; Pred. No. 4.7
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                                                                                                                                                                                                                                                                     EMBL; L24907; AAA19670.1; -.
EMBL; L26288; AAA66944.1; -.
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                     kinase IV
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RESULT 12
KCC4 HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                   MIM, 604949, 1

InterPro; IPR000290; Ser_thr_pkinase.

InterPro; IPR000290; Ser_thr_pkinase.

InterPro; IPR000290; Ser_thr_pkinase.

R Pfan, PP000000; Euk_pkinase; 1.

R PROSITE; RS00107; PROTEIN_KINASE_ATP; 1.

R PROSITE; PS00101; PROTEIN_KINASE_DOM; 1.

R PROSITE; PS00101; PROTEIN_KINASE_DOM; 1.

R PROSITE; PS00101; PROTEIN_KINASE_DOM; 1.

R PROSITE; PS00101; PROTEIN_KINASE_DOM; 1.

R PROSITE; PS00101; PROTEIN_KINASE_DOM; 1.

R PROSITE; PS00101; PROTEIN_KINASE_DOM; 1.

R Transferase; Serine/Chreonine-Protein; Kinase, Calmodulin-binding; PROPEIN KINASE PROMAIN 20 276 CALMODULIN-BINDING (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   138 VEACHSLGVWHRDLKPENFLFDSPKDDAKLKATDFGLSVFYKPGQYLYDVVGSPYYVAPE 197
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12 QAEDIRDIYDFRDVLGTGAFSEVILAEDKRTQKLVAIKCIAKEALEGKEG--SMENEIAV 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    249 AKDFIRHLMEKDPEKRFTCEQALQHPWIAGDTAL-DKNIHQSVSEQIKKNFAKSKWKQ 305
             -!- SUBUNIT: MONOMER.
-!- TISSUE SPECIFICITY: UBIQUITOUS.
-!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CAMK SUBFAMILY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .,
2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           55; Mismatches 114; Indels
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K->A: LOSS OF ACTIVITY.
57FA20ECE00FA76C CRC64;
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HSSP; Q63450; 1A06.
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                                                                                                                                                                                                                                                                                                                                                                              Genew; HGNC:1459; CAMK1.
MIM; 604998; -
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NP BIND
BINDING
ACT SITE
MOD RES
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Best Local
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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-:- SUBCELLULAR LOCATION: SUBSTANTIAL LOCALIZATION IN CERTAIN NEURONAL NUCLEI (BY SIMILARITY).
-:- ALTERNATIVE PRODUCTS: CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE TYPE IN CALAITIC CHAIN AND CALSPERMIN ARE OBFAINED BY ALTERNATIVE SPLICING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "A Ca2+/calmodulin-dependent protein kinase, CaM kinase-Gr, expressed after transformation of primary human B lymphocytes by Epstein-Barr virus (EBV) is induced by the EBV oncogene LMP1.", J. Virol. 68:1697-1705(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Strausberg R.; submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: CALSFERMIN IS A HEAT-STABLE, ACIDIC, CALMODULIN-BINDING PROTEIN.
XCC4 HUMAN STANDARD; PRT; 473 AA.
Q1656;
01-00V-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 41, Last annotation update)
15-UJN-2002 (Rel. 41, Last annotation update)
16-UJN-2012 (Rel. 41, Last annotation update)
CEC 2.7.1.123) (CAM kinase-GR) (CAMK IV).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. MEDILINE=94375404; PubMed=8089075; MEDILINE=94375404; PubMed=8089075; Kitani T., Okuno S., Fulisawa H.; "CDNA cloning and expression of human calmodulin-dependent protein "CDNA cloning and expression of human calmodulin-dependent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
TISSUE=Cerebellum, and Thymus;
MEDLINE=94252566; PubMed=8194751;
Bland N.M., Monroe R.S., Ohmstede C.A.;
"The cDNA sequence and characterization of the Ca2+/calmodulin-dependent protein kinase-Gr from human brain and
                                                                                                                                                                                                                                                                                         Homo sapiens (Human).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCSI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mosialos G., Hanissian S.H., Jawahar S., Vara L., Kieff E.,
Chatila T.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=94149862; PubMed=8107230;
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EMBL, L17000; AAA35393.1; --
EMBL; L24959; AAA18251.1; --
EMBL; BC016695; AAH16695.1; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  kınase 1V.";
J. Biochem. 115:637-640(1994).
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Genew; HGNC:1464; CAMK4.
MIM; 114080; -.
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Tobimatsu T., Fujisawa H.;
"Tisaue-specific expression of four types of rat calmodulin-dependent grants in ambas.";
J. Biol. Chem. 264:17907-17912(1989).
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                                                                                                                                                                                                                                                                                                                       82 SEHPNVVRIKGTYEDSVFVHIVMEVCEGGELFDRIVSKGHFSEREAVKLIKTILGVVEAC 141
                                                                                                                                                                                                                                                                                                                                              97 S-HPNIIKLKEIFETPTEISLVLELVTGGELFDRIVEKGYYSERDAADAVKQILEAVAYL 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Mētazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus
                                                                                                                                                                                                                                                                                                                                                                          HSLGVMHRDLKPENFLFDSPKDDAKLKATDFGLSVFYKPGQYLYDVVGSPYYVAPEVLKK 201
                                                                                                                                                                                                                                                                                       42 LSDFFEUESELGRGATSIVYRCKQKGTQKPYALKVLKK----TVDKKIVRTEIGVLLEL 96
                                                                                                                                                                                                                                                                       22 LRDHYLLGKKLGQGQFGTTYLCTEKSTSANYACKSIPKRKLVCREDYEDVWREIQIMHHL 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
15-UTM-2002 (Rel. 14, Last annotation update)
15-UTM-2002 (Rel. 14), Last annotation update)
15-UTM-2003 (Rel. 14), Last annotation update
15-UTM-1200 (Rel. 14), Last annotation (Cam kinase Lype II delta chain)
2.7.1.123) (Cam kinase II delta chain) (Cam kinase II delta subunit)
                                                                                                                                                                                                                                                                                                                                                                                          260 LIYKMLERSPKKRISAHEALCHPWIVDEQAAPDKPLDPAVLSRLKQFSQMNKIKKMALRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      334 VASSRLGSASSSHGSIQESHKASRDPSPIQDGNEDMKAIPEGEKIQGDGAQAAVKGAQAE
R InterPro; IPR000719; Euk_pkinase.
R InterPro; IPR002290; Ser_thr_pkinase.
R FroDom; P000069; pkinase; 1.
SMART; SM00220; Euk_pkinase; 1.
SMART; SM00220; Euk_pkinase; 1.
R PROSITE; PS00109; PROTEIN KINASE_ATP; 1.
R PROSITE; PS0011; PROTEIN KINASE_DOM; 1.
R PROSITE; PS0011; PROTEIN KINASE_DOM; 1.
R PROSITE; PS0011; PROTEIN KINASE_DOM; 1.
R Transferase; Serine/threonine-protein kinase; ATP-binding; Calmodulin-binding; 60 ATP (BY SIMILARITY).
I BIND 52 60 ATP (BY SIMILARITY).
I ACT SITE 164 164 BY SIMILARITY.
I DOWAIN 322 341 CALMODULIN-BINDING (POTENTIAL).
                                                                                                                                                                                                                    22.3%; Score 578.5; DB 1; Length 473; 37.2%; Pred. No. 2.1e-22; cive 65; Mismatches 144; Indels 27.
                                                                                                                               PROTEIN KINASE.
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY.
CALMODULIN-BINDING (POTENTIAL).
EFEESIES612326DC CRC64;
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Matches 140; Conservative
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                                                                                                                                                                                    322 3
473 AA;
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P15791;
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MEDLINE 93300844; PubMed-8390994; and Skeletal muscle; MEDLINE 93300844; PubMed-8390994; and Skeletal muscle; Schworer C.M., Rothblum L.I., Thekkumkara T.U., Singer H.A.; Schworer C.M., Rothblum L.I., Thekkumkara T.U., Singer H.A.; Schmodulin-dependent protein kinase II. Differential expression in rat brain and acrta."; J. Biol. Chem. 268:14443-1449(1993).

J. Biol. Chem. 268:14443-1449(1993).

J. CATALYTIC ACTIVITY: AFF + Brotein = APF + O-phosphoprotein.

J. CATALYTIC ACTIVITY: AFF + Brotein = APF + O-phosphoprotein.

J. SIDWIRT REGULATION: AUTOPHOSPHORYLATION OF CAM-KINASE II PLAYS AN IMPORTANT ROLE IN THE REGULATION OF THE KINASE ACTIVITY.

J. SIBUNIT: COMPOSED OF FOUR DIFFERENT CHAINS: ALPHA, BETA, GAMMA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nding; Neurone; Alternative splicing.
PROTEIN KINASE.
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY).
CALWODULIN-BINDING (BY SIMILARITY).
MISSING (IN ISOPORM DELTA 2).
INNYANV -> KRKSSSV (IN ISOPORM DELTA 3).
GNK -> QNM (IN ISOPORM DELTA 3).
GNK -> QNM (IN ISOPORM DELTA 3).
MISSING (IN ISOPORM DELTA 3).
MISSING (IN ISOPORM DELTA 3).
MISSING (IN ISOPORM DELTA 3).
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                                                                                                                                                                                                                                                                                                                                                                                                                            -: ALTERNATIVE PRODUCTS: 4 ISOFORMS; DELTA 1 (SHOWN HERE), DELTA 2, DELTA 3 AND DELTA 4; ARE PRODUCED BY ALTERNATIVE SPLICING.
-: TISSUE SPECIFICITY: DELTA 1 IS THE PREDOMINANT FORM IN THE BRAIN, DELTA 2 AND 3 PREDOMINATE IN THE AORTA AND DELTA 4 IN SKELETAL MUSCLE.
-: SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
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HSSP; Q63450; LA06.
InterPro; IPR001019; Euk_pkinase.
InterPro; IPR002019; Ser thr_pkinase.
Frobon; PP000001; Euk_pkinase; I.
PROSITE; PS00107; PROTEIN_KINASE_ATF; I.
PROSITE; PS00107; PROTEIN_KINASE_ATF; I.
PROSITE; PS00108; PROTEIN_KINASE_DON; I.
Transferase; Serine/Urreonine-protein kinase; Calmodulin-binding; Phosphorylation; ATP-binding; Neurone; Alernative splicing.
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EMBL; L13406; AAA41479.1; -.
EMBL; L13407; AAA41480.1; -.
EMBL; L13409; AAA41481.1; -.
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Matches 127; Conservative
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56
71
160
3337
337
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318
278
278
302
469 AA;
                                                                                                                                                                                                           Calmodulin-binding.
DOMAIN 42
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Best Local Similarity
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DOMAIN
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BINDING
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Proc. Nati. Acad. Sci. U.S.A. 84:3038-3042(1987).
-1- CATALYTIC ACTIVITY: ATP + protein = ADP + O-phosphoprotein.
-1- SUBCELLULAR LOCATION: SUBSTANTIAL LOCALIZATION IN CERTAIN NEURONAL
                                                                                                                                **ECC4 MOUSE STANDARD; PRT; 469 AA. 018414; Q61381; 01-4UG-1988 (Rel. 08, Created) 01-APR-1993 (Rel. 25, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) Calcium/calmodulin-dependent protein kinase type IV catalytic chain (EC 2.7.1.123) (CAM kinase-GR) (CaMK IV).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=87204263; PubMed=3033675; Sikela J.M., Hahn W.E.; Sikela J.M., Hahn W.E.; Screening an expression library with a ligand probe: isolation and sequence of a cDNA corresponding to a brain calmodulin-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                  -i- TISSUE SPECIFICITY: BRAIN AND TESTIS.
-i- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CAMK SUBFAMILY.
                     KK-CYGPEIDVWSAGVILYILLSGVPPFWAETESGIFRQILQGKLDFKSDPWPTISEAAK
                                                                                              DLIYKMLERSPKKRISAHEALCHPWIVDEQAAPDKPLDPAVLSRLKQFSQMNKIKKMALR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hahn W.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN=BABIS/C: TISSUE=Brain;
MEDINNE=BAIS/C: TISSUE=Brain;
Jones D.A., Glod J., Milson-Shaw D., Hahn W.E., Sikela J.M.;
"CDNA sequence and differential expression of the mouse
Ca24/calmodulin-dependent protein kinase IV gene.";
FEBS Lett. 289:105-109(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                [2]
SEQUENCE OF 240-469 FROM N.A.
SEQUENCE OF 240-469 FROM N.A.
MEDLINE=89122027; PubMed=2536634;
Sikels Barron Sequence of the human gene for brain "Chromosomal localization of the human gene for brain Ca2+/calmodulin-dependent protein kinase type IV.";
Genomics 4:21-27(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; M16206; AAA39933.1; --
EMBL; M64266; AAA37364.1; --
EMBL; J03057; AAA37366.1; --
EMBL; X58995; CAA41741.1; --
PIR; A29978; A29878.
                                                                                                                                                                                VIAERLSEEEIGGLKELFKMID 340
                                                                                                                                                                                                                      304 ILTIMLATRNFSAAKSLLKKPD 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   rissum=Brain;
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Rattus norvegicus (Rat).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi; Muridae, Murinae, Rattus.
[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              152 HENGIVHRDIKPENLIYATPAPDAPLKIADFGLSKIVEHOVLMKTVCGTPGYCAPELLRG 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     271
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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01-JAN-1990 (Rel. 13, Created)
01-JAN-1993 (Rel. 25, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
calcium/calmodulin-dependent protein kinase type IV catalytic chain (EC 2.7.1.123) (CAM kinase-GR) (CAMK IV) (Calspermin).
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ATP (BY SIMILARITY).
BY SIMILARITY.
CALMODULIN-BINDING (FOTENTIAL).
UD -> CGGI (IN REF. 2).
N -> T (IN REF. 2).
W, CEIF99670822F975 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 469;
MGD; MGI:88258; Camk4.
InterPro; IPR00019; Buk_pkinase.
InterPro; IPR00019; Buk_pkinase.
InterPro; IPR000290; Sar_thr_pkinase.
Ffam; PP000069; pkinase; I.
SWART; P0000001; Euk_pkinase; I.
PROSITE; PS00107; PROTEIN_XINASE_ATP; I.
PROSITE; PS00101; PROTEIN_XINASE_AT; I.
PROSITE; PS0011; PROTEIN_XINASE_DOM; I.
Transferase; Serine/threonine-protein kinase; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22.1%; Score 574; DB 1; Length 469
33.4%; Pred. No. 3.6e-22;
tive 79; Mismatches 170; Indels
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MEDLINE=96094352; PubMed=7493991;

Sun Z., Means R.L., LeMagneresse B., Means A.R.;

Sun Z., Means R.L., LeMagneresse B., Means A.R.;

protein kinase IV gene.";

J. Biol. Chem. 270:29507-29514(1995).

-i. FUNCTION: CAM KINASE GR IS A NEURONL-SPECIFIC PROTEIN KINASE,

BRRICHED IN CEREBELLAR GRANULE CELLS.

-i. FUNCTION: CALSPERMIN IS A HEAT-STABLE, ACIDIC, CALMODULIN-BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -1- CATALYTIC ACTIVITY: ATP + protein = ADP + 0-phosphoprotein.
-1- ALTERNATIVE PRODUCTS: 2 isoforms; 1/calcium-calmodulin-dependent protein kinase type IV catalytic chain (shown here) and 2/calspermin; are produced by alternative splicing.
-1- TISSUE SPECIFICITY: Isoform 1 is expressed in brain and isoform 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           is testis-specific.
-!- PTM: THE N-TERMINAL OF CALSPERMIN IS BLOCKED.
-!- MISCELLANDOUS: The presence of an alternative promoter gives rise to the testis-specific isoform 2/calspermin protein.
-!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
                                                                                                                                                                                                                                                                           MEDLINE=9104387; PubMed=1649385; Means A.R., Cruzalegui F., Lemagueresse B., Needleman D.S., Slaughter G.R., Ono T.; Indiana protein kinase and a male germ "A novel ca2+/calmodulin-dependent protein kinase and a male germ cell-specific calmodulin-binding protein are derived from the same
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 306-474 FROM N.A. (ISOFORM 2), AND SEQUENCE OF 335-361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=Sprague-Dawley;
MEDLINE-89132727; PubMed=2914893;
MODINE-89132727; PubMed=2914893;
ONO T. Slaughter G.R., Cook R.G., Means A.R.;
"Molecular clouing sequence and distribution of rat calspermin, a high affinity calmodulin-binding protein.";
J. Biol. Chem. 264:2087(1989).
SEQUENCE FROM N.A. (ISOPORMS 1 AND 2), AND PARTIAL SEQUENCE. MEDLINE=91288548; PubMed=1648230; Ohnstede C.-A., Bland M.M., Merrill B.M., Sahyoun N.; "Relationship of genes encoding C22+/calmodulin-dependent protein kinase Gr and calspermin: a gene within a gene."; Proc. Natl. Acad. Sci. U.S.A. 88:5784-5788(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 enriched in cerebellar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 250-474 FROM N.A. (ISOFORM 1).
STRAIN=Sprague-Dawley; TISSUB=Brain;
MEDLINE=89174647, PubMed=2538431;
Ohnstede C.-A., Jenson K.F., Sahyoun N.;
"Ca2+/calmodulin-dependent protein kinase enriched granule calls. Identification of a novel neuronal calmodulin-dependent protein kinase.";
J. Biol. Chem. 264:5866-5875(1989).
                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         thr pkinase.
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EMBL; M74488; AAA40855.1; ALT_SEQ.
EMBL; M64757; AAA40857.1; -.
EMBL; U04600; AAA41867.1; -.
EMBL; U04600; AAA41867.1; -.
EMBL; U04460; AAA41867.1; -.
EMBL; U0446; AAA41867.1; -.
EMBL; U0446; AAA41867.1; -.
EMBL; UR4501.190.1; -.
EMBL; UR4500.190.1; -.
EMBL; UR4886.1; -.
EMBL; UR4886.1; -.
EMBL; UR4886.1; -.
EMBL; UR4886.1; -.
EMBL; UR4886.1; -.
EMBL; UR4886.1; -.
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EMBL; UR4886.1; -.
EMBL; UR4886.1; -.
EMBL; UR4886.1; -.
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49 SANYACKSIPKRKLVCREDYEDVWREIQIMHHISEHPNVVRIKGTYEDSVFVHIVMEVCE 108
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CALMODULIN-BINDING (POTENTIAL).
POLY-GLU.
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SMART; SM00220; S.TKE; I.

PROSITE; PS00107; PROTEIN KINASE ATP; I.

PROSITE; PS00110; PROTEIN KINASE DOM; I.

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Transferase; Serine/threonine-protein kinase; ATP-binding; Calmodulin-binding; Testis; Alternative splicing.

Calmodulin-binding; Testis; Alternative splicing.

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A Goldsmith A.D., Jiang P.X., Lee J.M., Onodera C.S., Quach H.L.,
A Tang C., Toriumi M., Yamamura Y., Yu G., Yu S., Bowser L.,
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A Tang C., Toriumi M., Yamamura Y., Yim C., Koesema E., Lam B.,
A Carninci P., Chen H., Cheuk R., Mayani J., Kim C., Koesema E., Lam B.,
Lin J., Meyers M.C., Miranda M., Navusaka M., Nguyen M., Palm C.J.,
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NCBI_TaxID=3702;
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                                                                                                                                                                                                                                                                                                                                                                                                                      61 KLVCREDYEDVWREIQIMHHLSEHPNVVRIKGTYEDSVFVHIVMEVCEGGELFDRIVSKG 120
                                                                                                                                                                                                                                                                                                                                       1 METKPNPRRPSNTVLPYQTPRLRDHYLLGKKLGGGGFGTTYLCTEKSTSANYACKSIPKR 60
                                                                                                                                                                                                                                                                     1 METKPNPRRPSNTVLPYQTPRLRDHYLLGKKLGQGQFGTTYLCTEKSTSANYACKSIPKR 60
ATP-binding, Kinase, Serine/threonine-protein kinase, Transferase.
SEQUENCE 495 AA, 55867 MW, 5909A451242C3A6D CRC64;
                                                                                                                                                                                          .;
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                                                                                                           100.0%; Score 2593; DB 10; Length 495; 100.0%; Pred. No. 9.5e-183; ive 0; Mismatches 0; Indels 0;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MRA-2002 (TrEMBLrel. 20, Last annotation updat
Putative calcium-dependent protein kinase SK5.
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                                                                                                                                                 Best Local Similarity 100.
Matches 495; Conservative
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181 GQYLYDVVGSPYYVAPEVLKKCYGPEIDVWSAGVILYILLSGVPPFWAETESGIFRQILQ 240
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181 GQYLYDVVGSPYYVAPEVLKKCYGPEIDVWSAGVILYILLSGVPPFWAETESGIFRQILQ 240
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                                                                                                                                                                                                                                                                                                                                                                    99.4%; Score 2577; DB 10; Length 495; 99.6%; Pred. No. 1.4e-181; Live 0; Mismatches 2; Indels 0;
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                                                                                                                                                                                                                                                                                                         495 AA; 55916 MW; 2DD0ED8C234EF2F7 CRC64;
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
PFGAM, PPF00036; efhand, 4.
PEAM, PPF00009; Pkinase, 1.
Probom, PD000001; Euk pkinase, 1.
Probom; PD000001; EF-Fand; 2.
PROSITE: PS001018; EF-HAND; UNKNOWN 4.
PROSITE: PS00101; PROTEIN KINASE ATP; UNKNOWN 1.
PROSITE: PS00101; PROTEIN KINASE DOM; 1.
PROBITE: PS00108; PROTEIN KINASE ST; UNKNOWN 1.
PROBITE: PS00108; PROTEIN KINASE ST; UNKNOWN 1.
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4atches 493; Conservative
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                                                                                                                                                                                                                                                                                                         SEQUENCE
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Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.

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Query Match
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                                      Cheuk R., Shinn P., Brooks S., Buehler E., Chao O., Johnson-Hopson C., Khan S., Kin C., Altafi H., Bel B., Chin C., Chiou J., Choi E., Conn L., Conway A., Gonzalez A., Hansen N., Howing B., Koo T., Lem B., Lee J., Lenz C., Li J., Liu A., Liu J., Liu S., Mukharsky N., Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thaoveni A., Toriumi M., Vaysberg M., Yu G., Davis R., Federspiel N., Theologis A., Ecker J., Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databasses.
-- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES. HSSP, PO2593; 1FW4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97.8%; Score 2536; DB 10; Length 557; 88.5%; Pred. No. 1.8e-179;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ProDom; PD000001; ELK_Pkinase; 1.
ProDom; PD000001; ELK_Pkinase; 1.
SMART; SM00054; EFF, 4.
SWART; SM00020; STKc; 1.
SMOSITE; PS00019; FF HAND; UNKNOWN 4.
PROSITE; PS00010; PROTEIN KINASE APP; UNKNOWN_1.
PROSITE; PS00101; PROTEIN KINASE DOM; 1.
PROSITE; PS00108; PROTEIN KINASE DOM; 1.
ATP-binding; Scrinc/threonine-process ST; 1.
STRP-binding; Scrinc/threonine-process Kinase; Transferase.
SEQUENCE 557 AA; 63397 WW; 7E92BASA6B3A240B CRC64;
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                                                                                                                                                                                                                                                                                                                                                  Interpro; IPR002048; EP-hand.
Interpro; IPR00219; Euk pkinase.
Interpro; IPR00229; Ser thr pkinase.
Pfan; PF00036; efhand; 4.
Pfan; PF00069; pkinase; 1.
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Matches 493; Conservative
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
Spiegel L.A., Huang E.N., Nascimento L.U., de la Bastide M., Vil D.M.,
Spiegel L.A., Huang E.N., Shah R., O'Shaughnessy A., Rodriguez M.,
A preston R.R. Matero A., Shah R., O'Shaughnessy A., Rodriguez M.,
Shekher M., Schutz K., See L.H., Swaby I., Habermann K., Dedhia N.N.,
A Shekher M., Lemcke K., Mayer K.F.X.;
Shamitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
C L. SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
BRBL; U31722, AAB03243.1;
C L. SIMILARITY: BELONGS 11;
C SEMBL; ALIG131; CAB78000.1;
C SEMBL; ALIG131; CAB78000.1;
C SEMBL; ALIG131; CAB7800.1;
C SEMBL; ALIG131; CAB7800.1;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1996 (TrEMBLrel. 21, Last sequence update)
01-NOV-1996 (TrEMBLrel. 21, Last annotation update)
01-NOT-2002 (TrEMBLrel. 21, Last annotation update)
CRIMGOULIN-GOMAIN protein kinase CDPK isoform 4 (Fragment).
CRY4 OR T25P22.10 OR AT4GO8570.
Arabidopsis thaliana (Mouse-ear cress).
Arabidopsis thaliana (Mouse-ear cress).
Spermatophyta; Magnolliophyta; Euchtophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnolliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Exassicales; Brassicaceae; Arabidopsis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MCCOmbie R.W., Spiegel L.A., Huang E.N., Nascimento L.U., de la Bastide M., Vil D.M., Preston R.R., Matero A., Shah R., O'Shaughnessy A., Rodriguez M., Shekher M., Schutz K., See L.H., Swaby I., Habermann K., Dedhia N.N., Mewes H.W., Lemcke K., Mayer K.F.X., Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN=CV. COLUMBIA;
MCCOmble W.R.;
"Arabidopis thaliana Genomic Sequence, Chromosome IV.";
Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
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94.8%; Pred. No. 8.6e-173;
tive 9; Mismatches 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SMART; SMO0054; EPh, 4.

SMART; SMO0220; STKC; 1.

PROSITE; PSO010; FEPHND; UNKNOWN 4.

PROSITE; PSO010; PROTEIN KINASE ATP; UNKNOWN 1.

PROSITE; PSO010; PROTEIN KINASE DOM; 1.

PROSITE; PSO0108; PROTEIN KINASE ST; 1.

KINASE; SEINE/threonine-protein kinase.

SEQUENCE 501 AA; 56416 MW; C709CI7DFAF74B70
501 AA
PRT;
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Matches 470; Conservative
     PRELIMINARY;
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R InterPro; IPR0022048; EF-hand.

R InterPro; IPR0022049; EF-hand.

R InterPro; IPR0022049; EF-hand.

R InterPro; IPR0022049; EV. pkinase.

R InterPro; IPR002209; Ser thr pkinase.

Pfam; PF000069; pkinase; 1.

R Probom; PD000001; EUk pkinase; 1.

R PRODOM; PD000220; ET-hand; 2.

SMART; SM00024; EFh; 4.

R SMART; SM00024; EFF; 4.

R PROSITE; PS00010; PROTEIN KINASE ATP; UNKNOWN 1.

R PROSITE; PS00107; PROTEIN KINASE DOM; 1.

R PROSITE; PS00108; PROTEIN KINASE DOM; 1.

R PROSITE; PS00108; PROTEIN KINASE ST; 1.

R ATP-binding; Kinase; Serine/threonine-protein kinase; Iransferase.; ...

SEQUENCE 490 AA; 55164 MW; 2333C411CAA43E0F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     423 LQQACTEFGLCDTPLDDMIKEIDLDNDGKIDFSEFTAMMKKGDGVGRSRTMRNNLNFNIA 482
                                                     123 EREAAKLIKTILGVVEACHSLGVMHRDLKPENFLFDSPSDDAKLKATDFGLSVFYKPGQY 182
                                                                                                                                                                                                         183 LYDVVGSPYYVAPEVLKKCYGPBIDVWSAGVILYILLSGVPPFWAETESGIFRQILQGKI 242
                                                                                                                                                                                                                                                                                                                                                         243 DFKSDPWPTISEGAKDLIYKMLDRSPKKRISAHBALCHPWIVDEHAAPDKPLDPAVLSRL 302
124 EREAVKLIKTILGVVEACHSLGVMHRDLKPENFLFDSPKDDAKLKATDFGLSVFYKFGQY 183
                                                                                                                                           184 LYDVVGSPYYVAPEVLXKCYGPEIDVWSAGVILYILLSGVPPFWAETESGIFRQILQGKL 243
                                                                                                                                                                                                                                                                                                244 DFKSDPWPTISBAAKDLIYKWLERSPKKRISAHEALCHPWIVDEQAAPDKPLDPAVLSRL 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                304 KQFSQMNKIKKMALRVIAERLSBEBIGGLKELFKMIDTDNSGTITFEBLKAGLKRVGSEL 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      303 KQFSQMNKIKKMALRVIAERLSEEEIGGLKELFKMIDTDNSGTITFEELKAGLKRVGSEL 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    364 MESEIKSLMDAADIDNSGTIDYGEFLAATLHMNKMEREEILVAAFSDFDKDGSGYITIDE 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              363 MESEIKSLMDAADIDNSGTIDYGEFLAATLHINKMEREENLVVAFSYFDKDGSGYITIDE 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOSACTEFGLCDTPLDDMIKEIDLDNDGKIDFSEFTAMMRKGDGVGRSRTMMKNLNFNIA 483
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McKendree W.L., Doostdar H., McCollum T.G., Mayer R.T.;

McKendree W.L., Doostdar H., McCollum T.G., Mayer R.T.;

"cDNA cloning and expression of a gene (Accession No. 297064) from Citrus paradisi roots similar to bacterial YRN1 and HEAHIO proteins and an mRNA from Brassica oleracea that is wound and dark inducible (PGR97-127).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lee J.-Y., Yoo B.-C., Harmon A.C.;
Submitted (SEP-1996) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Calmodulin-like domain protein kinase isoenzyme beta.
Glycine max (Soybean).
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HSSP; P02588; 1PON.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            484 DAFGVDG----EKSDD 495
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O24430
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STRAINS CV. RIBHIRI; TISSUE=CELL SUSPENSION;
STRAINS CV. RIBHIRI; TISSUE=CELL SUSPENSION;
Calcium dependent protein kinase genes from resistant and susceptible potato cultivars to Phytophthora infestans.";
Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
BMBL; AB051809; BAB63464.1;
InterPro; IPR002049; EF-hand.
InterPro; IPR002049; EF-hand.
InterPro; IPR002049; FRY_PAinase.
InterPro; IPR001049; TY_PAinase.
Fram; PF00036; Efhand; 4.
Pfam; PF00036; Efhand; 4.
                                                                                                                                                                                                                                                                                                                  74 EIQIMHHLSEHPNVVRIKGTYEDSVFVHIVMEVÇEGGELFDRIVSKGHFSEREAVKLIKT 133
                                                                                                                                                                                                                                                                                                                                                                                           72 BIQIMHHLSEHPNVVQIQGTYEDSVFVHLVMELCAGGELFDRIIQKGHYSEREAAKLIKT 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       134 ILGVVEACHSLGVMHRDLKPENFLFDSPKDDAKLKATDFGLSVFYKPGQYLYDVVGSPYY 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                132 IVGVVEACHSLGVMHRDLKPENFLFDTPGEDAQMKATDFGLSVILQARQAFHDVVGSPYY 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 194 VAPEVLKKCYGPEIDVWSAGVILYILLSGVPPFWAETESGIFRQILQGKLDFKSDPWPTI 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         192 VAPBVICKQYGPEVDVWSAGVILYILLSGVPPFWAETEAGIFRQILNGDLDFVSEPWPSI 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          254 SEAAKDLIYKWLERSPKKRISAHBALCHPWIVDEQAAPDKPLDPAVLSRLKQFSQMNKIK 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     252 SENAXELVKQMLDRDPKKRISAHEVLCNPWVVDD-IAPDKPLDSAVLTRLKHFSAMNKLK 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               314 KWALRVIAERLSEEBIGGLKELFKMIDTDNSGTITFEELKAGLKRVGSELMESEIKSLMD 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   311 KMALRVIAERLSEEEIGGLKELFKMIDTDNSGTITFEELKEGLKSVGSNLMESEIKSLME 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         374 AADIDNSGTIDYGEFLAATLHMNKMEREEILVAAFSDFDKDGSGYITIDELQSACTEFGL 433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        371 AADIDNNGSIDYGEFLAATLHLNKMEREENLVAAFAYFDKDGSGYITIDELQQACKDFSL 430
                                                                                2; Gaps
                                                                                                                                                                                                                12 VLPYQTARLRDHYVLGKKLGQQQPGTTYLCTHKVTGKLYACKSIPKRKLMCQEDYDDVWR 71
                                                                                                                                                         14 VLPYQTPRLRDHYLLGKKLGQGQFGTTYLCTEKSTSANYACKSIPKRKLVCREDYEDVWR 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
Asteridae, euasterids I, Solanales, Solanaceae, Solanum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  434 CDTPLDDMIKEIDLDNDGKIDFSEFTAMMRKGD-GVGRSRTMMKNLNFNIADAFGV 488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             431 GDVHLDEMIKEIDQDNDGRIDYAEFAAMMKKGDPNMGRSRTMKGNLNFNIADAFGM 486
Query Match 78.3%; Score 2030; DB 10; Length 490; Best Local Similarity 81.1%; Pred. No. 2.8e-141; Matches 386; Conservative 43; Mismatches 45; Indels 2.
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Last annotation update)
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Probon; PD000001; EF-hand; 2.

SMART; SM00219; TYKK; 1.

PROSITE; PS00109; EF HAND; UNKNOWN 4.

PROSITE; PS00107; PROTEIN KINASE_ATP; UNKNOWN_1.

PROSITE; PS00109; PROTEIN KINASE_DOM; 1.

ATP-binding; Kinase; Transferase.
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01-DEC-2001 (TrEMBLrel. 19, Last sequ
01-MAR-2002 (TrEMBLrel. 20, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Calcium dependent protein kinase.
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Q93XI9
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SEQUENCE Query Match Best Local

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421 IDBLQSACTEFGLCDTPLDDMIKEIDLDNDGKIDFSEFTAMMRKGDGVGRS---RTWMKN 477
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-UND-2002 (TrEMBLrel. 21, Last annotation update)
08CDPR7.
0rSCDPR7.
0ryza sativa (Rice).
0ryza sativa (Rice).
0ryza sativa (Nice).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SRLKKFSAMNKLKKWALRVIAERLSBEBEIGGLKELFKMIDTDKSGTITFEELKDSMRRVG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             301 SRLKQFSQMNKIKKMALRVIAERLSBEBIGGLKELFKMIDTDNSGTITFBELKAGLKRVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         417 IEBLĄQAMKEFGINDSNLDEMIKDIDQDNDGQIDYGEFVAMMRKGNGTGGGIGRRTMRNS
                                                                                                                                                                             Prodom; PD00001; Euk_pkinase; 1.
SMART; SM00054; EF-hand; 2.
SMART; SM00054; EF-hand; 2.
SMART; SM00220; S_TKc; 1.
SMART; SM00220; S_TKc; 1.
PROSITE; PS00101; EF_HAND; UNKNOWN 4.
PROSITE; PS00101; PROTEIN KINASE ATP; UNKNOWN 1.
PROSITE; PS00101; PROTEIN KINASE DOM; 1.
ATP-binding; Kinase; Sexine/threomine-protein kinase; Transferase.
SROUBNC 490 AA, S5379 MW; 0315346396585264 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 KLVCREDYEDVWREIQIMHISEHPNVVRIKGTYEDSVFVHIVMEVCEGGELFDRIVSKG
SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES
                                                                                                                                                                                                                                                                                                                                                                              DB 10; Length 490;
                                                                                                                                                                                                                                                                                                                                                                                                                 68; Indels
                                                                                                                                                                                                                                                                                                                                                                           Query Match
71.1%; Score 1844.5; DB 1C
Best Local Similarity 73.1%; Pred. No. 1.3e-127;
Matches 353; Conservative 55; Mismatches 68;
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                   EMBL; U20626; AAA67657.1; -...
EMBL; U20389; AAA67653.1; -...
EMBL; ABA02563; BAA97242.1; -...
HSSP; P02589; 1PON.
InterPro; IPR002048; EF-hand.
InterPro; IPR000719; Buk pkinase.
InterPro; IPR002290; Ser_thr_pkinase.
Pfam; PF00069; pkinase; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1996 (TTEMBLrel. 01, Created)
01-NOV-1996 (TTEMBLrel. 01, Last sequence update)
01-NOV-1996 (TTEMBLrel. 20, Last annotation update)
01-MAR-2002 (TTEMBLrel. 20, Last annotation update)
01-MAR-2002 (TTEMBLrel. 20, Last annotation update)
02-DPX9.
Arabidopsis thaliana (Mouse-ear cress).
Arabidopsis thaliana (Mouse-ear cress).
Spermatophyta; Wagnollophyta; eddicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NRBL TAXID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            358
                                                                                                                                                                                                                                                                                                                                                                   240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-COLUMBIA;
Hong Y., Takano M., Liu C.M., Gasch A., Chye M.L., Tan C.T., Koh C.C.
Chua N.H.;
                                                                                                                                                                                                                                                          178
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                                                                                                                                                                                                                                                                                                                                                                                                       298
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                                                                                                                                                                                                          61 KKKLICKEDYEDVWKEIQIMHHLSEHPNVVRIKGTYEDALYVHIVMELCAGGELFBIVE 120
                                                                                                                                                                                                                                                                                              180
                                                                                                                                                                                     59 KRKLVCREDYEDVWREIQIMHHLSEHPNVVRIKGTYEDSVFVHIVMEVCEGGELFDRIVS 118
                                                                              Gaps
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                                                                                                              1 METKP--NPRRPSNTVLPYQTPRLRDHYLLGKKLGQGQFGTTYLCTEKSTSANYACKSIP
                                                                                                                                     KGHFSEREAVKLIKTILGVVEACHSLGVMHRDLKPENFLFDSPKDDAKLKATDFGLSVFY
                                                                                                                                                                                                                                                                               KPGQYLYDVVGSPYYVAPEVLKKCYGPEIDVWSAGVILYILLSGVPPFWAETESGIFRQI
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Sato S., Nakamura Y., Kaneko T., Katoh T., Asamizu E., Kotani H.
Tabata S.;
                                                                              7:
                                           DB 10; Length 496;
                                                                                53; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               to the EMBL/GenBank/DDBJ databases
         55774 MW; EC41F7AED33B6DDS CRC64;
                                          76.0%; Score 1969.5; DB 10
76.6%; Pred. No. 8.3e-137;
                                                                                55; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          490
                                                                                  Conservative
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NL--NLGEALGL 489
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             496 AA;
                                                                Similarity
                                                                  Best Local Sim
Matches 377;
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Q42396 Q42396;

RESULT 7 042396

240 236 300

116 180 176

56

360 356 420 416 476

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  195 IIVGVVEACHSLGVMHRDLKPENFLLANKDDDLSLKAIDFGLSVFFKFGGTFTDVVGSFY 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    193 YVAPEVLKKCYGPEIDVWSAGVILYILLSGVPPFWAETESGIFRQILQGKLDFKSDPWPT 252
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               375 KKMALRVIAESLGEEEBIAGLKEMFQIMDADNSGAITYDELKEGLRKYGSTLKDTEIRDLM 434
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2; Gaps
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                                                                                                                                                                                                                                  Saijo Y., Hata S., Kyozuka J., Shimamoto K., Izui K.;
"Over-expression of a single Ca2+-dependent protein kinase confers
both cold and sallt/drought tolerance on rice plants.";
Plant J. 23:319-327(2000).
EMBL; AB042550; BAB16888.1;
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
NCBI_TaxID=4530;
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                                                                                                                              SEQUENCE FROM N.A.
STRAIN-CV. NIPPONBARE;
MEDLINE-20387027; Pubmed=10929125;
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004417; 01-JUL-1997 (TrEMBLrel. 04, Created)

PRELIMINARY;

RESULT 9 004417 ID 004417

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Zea mays (Maize).
Zea mays (Maize).
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
Panicoideae; Andropogoneae; Zea.
NCBI_TaxID=4577;
                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN=RONEY BANTUN;
MEDLINE=97294505; PubMed=9150261;
Berberich T., Kusano T.;
"Cycloheximide induces a subset of low temperature-inducible genes in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          373 DAADIDNSGTIDYGEFLAATLHMNKMBREEILVAAFSDFDKDGSGYITIDELQSACTEFG 432
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                                                                                                                                                                                                                                                                             Berberich T., Kusano T.;
"Cycloheximide induces a subset of low-temperature-inducible genes in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           193 YVAPBVLKKCYGPEIDVWSAGVILYILLSGVPPFWABTESGIFRQILQGKLDFKSDPWPT 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        73 REIQIMHHLSEHPNVVRIKGTYEDSVFVHIVMEVCEGGELFDRIVSKGHFSEREAVKLIK 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 67.6%; Score 1752; DB 10; Length 492; Best Local Similarity 70.6%; Pred. No. 8.7e-121; Matches 334; Conservative 54; Mismatches 83; Indels. 2; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13 TVLPYQTPRIRDHYLLIGKKLGQGQFGTTYLCTEKSTSANYACKSIPKRKLVCREDYEDVW 72
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mol. Gen. Genet. 254:275-283(1997).
-:- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES
01-JUL-1997 (TrEMBLrel. 04, Last sequence update) 01-MAR-2002 (TrEMBLrel. 20, Last annotation update) Calcium dependent protein kinase.
                                                                                                                                                                                                                                                                                                                                            Mol. Gen. Genet. 0:0-0(1996).
                                                                                                                                                                                                                                                            STRAIN-HONEY BANTUM;
                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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Query Match
Best Local Similarity 70.0%
Matches 333; Conservative
                                                                                                                                                                  PRELIMINARY;
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STRAIN=INBRED LINE H84;
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R InterPro; IPR002048; EF-hand.
R InterPro; IPR00219; Euk_pkinase.
R InterPro; IPR00219; Euk_pkinase.
R InterPro; IPR00219; Euk_pkinase.
R Pfam; PF00005; Pfand; 4.
R ProDom; PF000001; Euk_pkinase; 1.
R ProDom; PF000012; EF-hand; 2.
R SMART; SM00250; S TKC; 1.
R PROSITE; PS00101; PROTEIN KINASE ATP; UNKNOWN 4.
R PROSITE; PS001019; PROTEIN KINASE DOM; 1.
R PROSITE; PS001019; PROTEIN KINASE DOM; 1.
R PROSITE; PS001018; PROTEIN KINASE DOM; 1.
R PROSITE; PS001018; PROTEIN KINASE SEQUENCE 487 AA, 54700 MW; 54E6FBF5D93ABBC2 CRC64;
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                                                                                                                                                                                              Phaseolus aureus (Mung bean) (Vigna radiata).
Eukaryota, Viridiplantae, Streptophyta, Embryophyta; Tracheophyta;
Spermatophyta; Magnaliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Vigna.
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374 DAADIDNSGTIDYIEFIAATLHLNKLEREEHLVAAFSYFDKDGSGYITVDELQLACKEHN
                                                                                                                                                                                                                                                          433 LCDTPLDDMIKEIDLDNDGKIDFSEFTAMMRKGD-GVGRSRTMMKNLNFNIAD 484
                                      67.5%; Score 1751; DB 10; Length 487; 69.1%; Pred. No. 1e-120; ive 64; Mismatches 80; Indels 2
                                                                                                                       Q43676;
01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NN-2002 (TrEMBLrel. 20, Last annotation update)
Calcium dependent protein kinase.
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Matches 327, Conservative
                                                                                                            PRELIMINARY;
                                                                                                            043676
                                                                                     RESULT 10
Q43676
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Zea mays (Maize).
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
Panicoideae; Andropogoneae; Zea.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           73 REIQIMHHLSEHPNVVRIKGTYEDSVFVHIVMEVCEGGELFDRIVSKGHFSEREAVKLIK 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13 TVLPYQTPRLRDHYLLGKKLGGGGFGTTYLCTEKSTSANYACKSIPKRKLVCREDYEDVW 72
                                                                    374 AADIDNSGTIDYGEFLAATLHMNKMEREEILVAAFSDFDKDGSGYITIDELQSACTBFGL 433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       198 IIVGVVEACHSLGUMHRDLKPENFLLVNKDDDLSLKAIDFGLSVFFKPGQVFTDVVGSPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SMART; SM00054; EFH; 4.

SMART; SM00020; S TKC; 1.

PROSITE; PS00010; PEF HAND; UNKNOWN 4.

PROSITE; PS00010; PROTEIN KINASE ATP; UNKNOWN 1.

PROSITE; PS00010; PROTEIN KINASE DOM; 1.

PROSITE; PS00100; PROTEIN KINASE DOM; 1.

ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase. SEQUENCE 554 AA; 61056 MM; 51FC6F44684C57C6 CRC64;
312 KWALRVIAESLSEEBIAGLREMFQAMDTDNSGAITFDELKAGLRRYGSTLKDVEINBLME
                                                                                                 67.3%; Score 1745; DB 10; Length 554; 70.0%; Pred. No. 3.4e-120;
                                                                                                                                                                434 CDTPLDDMIKEIDLDNDGKIDFSEFTAMMRKGD-GVGRSRTMMKNLNFNIADA
                                                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Pred. No. 3.4e
57; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR002048; EF-hand.
InterPro; IPR002049; EW_pkinase.
InterPro; IPR002190; Ser_thr_pkinase.
Pfam; PP00036; efhand; 4.
Pfam; PP000069; pkinase; 1.
ProDom; PD000001; EW_pkinase; 1.
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R EMBL; U31834; AAB03245.1; -.

R EMBL; AL022604; CAA48738.1; -.

R EMBL; AL022604; CAA48738.1; -.

R EMBL; AL022604; CAA60248.1; -.

R EMBL; AL022604; EF-hand.

R InterPro; IPR002049; EF-hand; 4.

R Pfam; PF000069; pkinase; 1.

R Pfam; PF000069; pkinase; 1.

R Probom; PD000001; EPh; 4.

R PROBITE; SM00029; EF-hand; 2.

R RART; SM00020; EF-hand; 2.

R RART; SM00109; PROFEIN KINASE AFP; UNKNOWN 4.

R PROSITE; PS0011; PROFEIN KINASE DOM; 1.

R PROSITE; PS00101; PROFEIN KINASE DOM; 1.

R ROSITE; PS00101; PROFEIN KINASE ST; 1.

R ROSITE; PS00109; PROFEIN KINASE ST; 1.

R ROSITE; PS00109; PROFEIN KINASE ST; 1.

R ROSITE; PS00109; PROFEIN KINASE ST; 1.

R RAP-binding; Kinase; Seriae (hrechine-protein kinase; Transferase.)

R REQUENCE SS6 AA; 6127 MW; 737FIADD582B45ED CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
Bevan M., Hilbert H., Braun M., Holzer E., Brandt A., Duesterhoeft A.,
Hobeisel J., Jesse T., Heijnen L., Vos P., Mewes H.W., Mayer K.F.X.,
Schueller C.,
Submitted (APR-1998) to the EMBL/GenBank/DDbJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Viridiplantae; Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons; core eudicots; Rosidae, eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                           373 DAADIDNSGTIDYGEFLAATLHMNKMEREEILVAAFSDFDKDGSGYITIDELQSACTEFG 432
                                                                                                                              313 KKWALRVIAERLSEEBIGGLKELFKMIDTDNSGTITFEELKAGLKRVGSELMESEIKSLM 372
                                                                 BU Arabidopsis sequencing project;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY; BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
                                                                                                                                                                      433 LCDTPLDDMIKEIDLDNDGKIDFSEFTAMMRKGD-GVGRSRIMMKNLNFNIADAFG 487
                                                                                                                                                                                          67.2%; Score 1742; DB 10; Length 556; 68.4%; Pred. No. 5.7e-120;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
Hilbert H., Braun M., Holzer E., Brandt A., Duesterhoeft A.
Mewes H.W., Lemcke K., Mayer K.F.X.;
Submitted (MAK-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STEAIN-COLUMBIA;
Hrabak E.M., Dickmann L.J., Satterlee J.S., Sussman M.R.,
Submitted (JUL-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                              01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NAR-2002 (TrEMBLrel. 02, Last annotation update)
62-Madulin-domain protein kinase CDFK isoform 5.
CPKS OR F23E12.130 OR AT4G35310.
Arabidopsis thaliana (Mouse-ear cress).
                                                                                                                                                                                                                                                                                    556 AA
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Q38871
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Query Match Best Local Similarity

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SEQUENCE FROM N.A.
STATIS=CV. RISHIRI, TISSUE=SUSPENSION CULTURE;
STRAIN=CV. RISHIRI, TISSUE=SUSPENSION CULTURE;
STRAIN=CV. RISHIRI, TISSUE=SUSPENSION CULTURE;
TUTUTION N. O'NUTA T., Hara N.;
TCalcium dependent protein kinase genes from resistant and susceptible acts cultivars to Phytophthoza infestans.";
TO Extra CONTRIVATE TO PHYTOPHTHOZA INFESTANS.";
SUBMIT ABOSISOS; BAB63463.1;
INTERPRO; IPRO02296; BEL, PAING.
INTERPRO; IPRO02296; BEL, PAING.
INTERPRO; IPRO03296; Ser_thr_pkinase.
INTERPRO; IPRO0369; EARANG, 1.
PRODOM; POTOMOSI; EFRANG, 1.
PRODOM; POTOMOSI; EFRANG, 1.
PROSITE; PSO0107; PROTEIN KINASE ATP; UNKNOWN.1.
PROSITE; PSO0107; PROTEIN KINASE DOM; 1.
PROSITE; PSO0107; PROTEIN KINASE DOM; 1.
PROSITE; PSO0108; PROTEIN KINASE ST; UNKNOWN.1.
2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         366 SEIKSIMDAADIDNSGTIDYGEFLAATLHMNKWEREEILVAAFSDFDKDGSGYITIDELQ 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  426 SACTEFGLODTPLDDMIKEIDLDNDGKIDFSEFTAMMRKGD-GVGRSRTWMKDLNFNIAD 484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BAVKLIKTILGVVBACHSLGVMHRDLKPENFLFDSPKDDAKLKATDFGLSVFYKPGQYLY 185
                                                                                                                                                                                                                                                                      246 KSDPWPTISEAAKDLIYKWLERSPKKRISAHEALCHPWIVDEQAAPDKPLDPAVLSRLKQ 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                           77 NPDNQAYYVLGHKTPNIRDIYTLSRKLGQGQFGTTYLCTBIASGVDYACKSISKRKLISK 136
                                                                                                                                         EDYEDVWREIQIMHHLSEHPNVVRIKGTYEDSVFVHIVMEVCEGGELFDRIVSKGHFSER 125
                                             NPRRPSNTVLPYQTPRLRDHYLLGKKLGQGQFGTTYLCTEKSTSANYACKSIPKRLVCR 65
  Gaps
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3
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Last annotation update)
     84;
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     66; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-DEC-2001 (TrEMBLrel. 19, 01-DEC-2001 (TrEMBLrel. 19, 01-MAR-2002 (TrEMBLrel. 20,
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          Matches 329; Conservative
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226

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01-NOV.1996 (TERMBLEAL. 01, Created)
01-NOV-1996 (TERMBLEAL. 01, Last sequence update)
01-NAR-2002 (TERMBLEAL. 20, Last sequence update)
01-NAR-2002 (TERMBLEAL. 20, Last sequence Calmodulin-domain protein kinase CDPK isoform 6.
CPK6 OR F36.5.
CPK6 OR F36.5.
Endatopsis thaliana (Mouse-ear cress).
Endatopsis thaliana (Mouse-ear cress).
Endatopsis thaliana (Mouse-ear cress).
Endatopsis thaliana (Mouse-ear cress).
Spermatophyta; Magnoliophyta; endicotyledons; core endicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ITFBELKAGLKRVGSELMBSEIKSLMDAADIDNSGTIDYGEFLAATLHMNKMEREEILVA 406
                                                                                                                                                                                                                                                                                                                                                                                                   47 STSANYACKSIPKRKLVCREDYEDVWRBIQIMHHLSEHPNVVRIKGTYEDSVFVHIVMEV 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                107 CEGGELFDRIVSKGHFSEREAVKLIKTILGVVEACHSLGVMHRDLKPENFLFDSPKDDAK 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               167 LKATDFGLSVFYKPGQYLYDVVGSPYYVAPEVLKKCYGPEIDVWSAGVILYILLSGVPPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     227 WAETESGIFROILOGKLDFKSDPWPTISEAAKDLIYKWLERSPKKRISAHEALCHPWIVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EQAAPDKPLDPAVLSRLKQFSQMNKIKKMALRVIAERLSEEEIGGLKELFKMIDTDNSGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              407 AFSDFDKDGSGYITIDELQSACTEFGLCDTPLDDMIKEIDLDNDGKIDFSEFTAMMRKGD
                                                                                                                                                                                                                                                                                      2 ETKPNPRRP------SNTVLPYQTPRLRDHYLLGKKLGQGQFGTTYLCTEK
                                                                                                                                                                      Query Match
Best Local Similarity 67.4%; Pred. No. 2.6e-119;
Matches 325; Conservative 62; Mismatches 80; Indels 15;
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to the EMBL/GenBank/DDBJ databases.
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to the EMBL/GenBank/DDBJ databases
PROSITE; PSO0107; PROTEIN KINASE AIP; UNKNOWN_1.
PROSITE; PSO0101; PROTEIN KINASE_DOM; 1.
PROSITE; PSO0108; PROTEIN KINASE_ST; UNKNOWN_1.
AIP-binding; Kinase; Transferase.
STR AA; 64723 MW; 88778B73F85A16B6
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STRAIN-CV. COLUMBIA,
Shong J.M., Ma P.N., P.
Submitted (JUL-1997) tv
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Submitted (JUL-1996) t
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Q38872
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SEQUENCE FROM N.A.

A ROBELS T., Ludwig A.A., Martin R., Jones J.D.G.;

AR Calcium-dependent protein kinases play an essential role in a plant defence response.";

R defence response.";

EMBJ, AJ344155, CA682999.1;

DR EMBJ, AJ344155, CA682999.1;

DR InterPro; IPR0021049; EF-hand.

DR InterPro; IPR00219; EF-hand.

DR Propo, PR00031; EF-hand.

DR Propom; P000069; pkinase. 1.

DR ProDom; P000001; Euk_pkinase. 1.

DR PROSITE; PS00018; EF-HAND; UNKNOWN_4.
                                                                                                                                                                                                                          CEGGELFDRIVSKGHFSEREAVKLIKTILGVVEACHSLGVMHRDLKPENFLFDSPKDDAK 166
                                                                                                                                                                                                                                                                                                                                                                                                                                              LKATDFGLSVFYKPGQYLYDVVGSPYYVAPEVLKKCYGPEIDVWSAGVILYILLSGVPPF 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WAETESGIFRQILQGKLDFKSDPWPTISEAAKDLIYKMLERSPKKRISAHEALCHPWIVD 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              346
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Nicotiana tabacum (Common tobacco).
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons; core eudicots;
Asteridae, euasterids I; Solanales; Solanaceae; Nicotiana.
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                                                                                                                                                                                     ETXPNPRRP-----SNTVLPYQTPRLRDHYLLGKKLGQGQFGTTYLCTEK
                                                                                                                               15;
                                                                        DB 10; Length 578;
                                                                     67.1%; Score 1739.5; DB 10; Lengt! 67.6%; Pred. No. 9.3e-120; active 62; Mismatches 79; Indels
                  64779 MW; 1009FF973EB662D2 CRC64;
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COSTYF3:
COLDEC-2001 (TrEMBLrel. 19, Created)
O1-DEC-2001 (TrEMBLrel. 19, Last sequence update)
O1-DEC-2002 (TrEMBLrel. 19, Last sequence update)
Calcium-dependent protein kinase 3.
CDPX3.
                                                                           Query Match
Best Local Similarity 67.6
Matches 326; Conservative
                        578 AA;
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RESULT 14 Q93YF3

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              306 PSQWNKIKKWALRVIAERLSEEEIGGLKELFKMIDTDNSGTITFEELKAGLKRVGSELME 365
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Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
L submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
R BEBL; U31835; AAB63246.1; -.
R EMBL; DAC02329; AAB86506.1; -.
R HASP; PO2593; LCTR.
R InterPro; IPR000248; EF-hand.
R InterPro; IPR000719; EUK_Dkinase.
R InterPro; IPR000719; EUK_Dkinase.
R Pfam; PF000036; efhand; 4.
R Pfam; PF000036; efhand; 4.
R Probom; PD000001; ENK_Dkinase; 1.
R Probom; PD000012; EF-hand; 2.
R SMART; SM00024; EFh; 4.
R PROSTIE; PS00107; PROTEIN KINASE AFP; UNKNOWN_1.
R PROSTIE; PS00107; PROTEIN KINASE AFP; UNKNOWN_1.
R PROSTIE; PS00107; PROTEIN KINASE ST; N;
R PROSTIE; PS00107; PROTEIN KINASE ST; N;
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Best Local Similarity 68.3%; Pred. No. 3.6e-119;
Matches 328; Conservative 65; Mismatches 85; Indels 2
                                                                                                             SEQUENCE FROM N.A.
STRAIN=CV. COLUMBIA;
Zhong J.M., Ma P.N., Parnell L.D., Chen C.-N., Chen E.Y.;
Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
STRAIN=CV. COLUMBIA;
Parnell L., McCombie W.R.;
Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.
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STRAIN=CV. COLUMBIA;
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(without alignments)
10976.382 Million cell updates/sec
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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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Perfect score:
Sequence:
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Result % Core Match Length DB ID 1	Description	15396 Arabid 15398 Arabid 152 Arabid 152 Arabid 151809 Solunia 151809 Solunia 151809 Solunia 151809 Solunia 151809 Solunia 151809 Solunia 151809 Cucurb 151801 C	mRNA linear PLN 05-FEB-1999 cium-dependent protein kinase ATCDFX2. mbla) cDNA to mRNA. phyta; Embryophyta; Tracheophyta; icotyledens; ore eudicots; hassicaceae; Arabidopsis. ; Brassicaceae; Arabidopsis.
Score Match Length DB 1171 1000 1147 8 1171 1000 1147 8 1171 1000 1147 8 1171 1000 1147 8 1171 1000 1147 8 1171 1000 1175 8 1171 10		LN	1747 bp NA for cal in kinase; strain:Colu strain:Strepto phyta; eud phyta; eud strassicales
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/tränslation="METKPNPRRPSNTVLPYQTPRLRDHYLLGKKLGQQQFGTTYLCT
ERSTSNAYACKSIPKRKTVCREDYEDDWRELQIMHLLSEPHYVBLKTYEDSVPHT
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PKDDAKLKATDFGLSVFYKPQQYLYDVVGSPYYVAPEVLKKCYGPEIDWWSAQVILYI
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BALCHPWIVDEQAAPDKPLDPAVLSRLKQFSQMNKIKKMALRVIAERLSEBEIGGLKE
LFKMIDTDNSGTITFBELKAGLKRVGSELMESEIKSLMDAADIDNSGTIDYGEFLAAT
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GKIDFSEFTAMMEKGDGVGRSRTMMKNLNFNIADAFGVDGEKSDD"
order (500. .531, complement (1301. .1323))
/gene="ATCDPK2"
                        Two genes that encode Ca(2+)-dependent protein kinases are induced by drought and high-salt stresses in Arabidopsis thaliana Mol. Gen. Genet. 244 (4), 331-340 (1994)
                                                                                                                                                                   Direct Submission
Submitted (30-OCT-1993) Kazuo Shinozaki, Tsukuba Life Science
Submitted (30-OCT-1993) Kazuo Shinozaki, Tsukuba Life Science
Center, The Inst. of Physical and Chemical Res.; 3-1-1 Kohyadai,
Tsukuba, Ibaraki 350, Japan (E-mail:sinozaki@rtcs1.riken.go.jp,
Tel:0298-36-4359, Fax:0298-36-9060)
On Mar 22, 1996 this sequence version replaced g1:540482.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           240
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/protein_id="BAA04830.1"

    1747
    organism="Arabidopsis thaliana"

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Hayashida, N. and Shinozaki, K.
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                                            421 AAAGGTCATTTTAGTGAGCGTGAAGCTGTCAAGCTTATTAAGACGATTCTTGGTGTTGTT
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VMEVCBGGELPDRIVSKGHYSBREAVKLIKTLGVVBACHSGRYNRDLKPENFLFDS
PKDDAKLKATDFGLSVRFRQQYLDTVVGSPYYAPABVLKKCYGPBIDVWSAGVILYI
LLSGVPPFWARTESGIFRQILGGKLDFKSDPWFITSBAACDLIYKMLBREBEBIGGLKE
BALCHPWIVDBQAAPDKPLDPAVLSRLKGSGWNKIKKMALRVIABRLSEBEBIGGLKE
LFKMIDTNNGGTITPEBLAGLKAGLKRVSELMESBIKGLMDAADIDNGGTIDYGBFLAAT
LHMWKMFREENLVAAFSYFDKDGSGYITIDELQSACTEFGLCDTPLDDMIKEIDLDND
Yamada,K. (SSP/PGEC) and Seki,M. (RIKEN GSC) contributed equally this work. Shinozaki,K. (RIKEN GSC) and Theologis,A. (SSP/PGEC) contributed equally to this work as PIs.
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| Gene="At1g35670"
|/note="contains a protein kinase PF00069 domain and
contains 4 EF hand PF00036 domains"
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/note="This clone is in a modified
(FLC-1) as a BamHI/XhoI insert.
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/chromosome="1"
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae, eurosids II; Brassicales; Brassicaceae, Arabidopsis.

E 1 (bases 1 to 1750)
S yamada,K., Liu,S.X., Sakano,H., Pham,P.K., Banh,J., Chung,M.K.,
Goldamith,A.D., Lee,J.W., Quach,H.L., Toriumi,M., Yu,G., Bowser,L.,
Jones,T., Kamnya,A., Karlin-Neumann,G., Kawai,J., Kim,C., Lam,B.,
In,J., Miranda,M., Narusaka,M., Nguyen,M., Palm,C.J., Sakurai,T.,
Satou,M., Seki,M., Shinn,P., Southwick,A., Shinozaki,K.,
Davis,R.W., Ecker,J.R. and Theologis,A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Arabidopsis thaliana putative calcium-dependent protein kinase AX050981
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Yamada, K., Liu, S.X., Pham, P.K., Banh, J., Banno, F., Dale, J.M.,
Yamada, K., Liu, S.X., Pham, P.K., Banh, J., Banno, F., Quach, H.L.,
Goldsmith, A.D., Jiang, P.X., Lee, J.M., Onodera, C.S., Quach, H.L.,
Tang, C.C., Toriumi, M., Yamamura, Y., Yu, G., Yu, S., Bowser, L.,
Carninci, P., Chen, H., Cheuk, R., Hayashizaki, Y., Ishida, J.,
Kones, T., Kamiya, A., Karlinn Neumann, G., Kawai, J., Kim, C.,
Koesema, E., Lam, B., Lin, J., Meyers, M.C., Miranda, M., Narusaka, M.,
Nguyen, M., Palm, C.J., Sakurai, T., Satou, M., Seki, M., Shinn, P.,
Phonia and M., Palm, C.J., Sakurai, T., Satou, M., Boki, M., Shinn, P.,
Phonia and M., Palm, C.J., Sakurai, T., Satou, M., Davis, R.W., Ecker, J.R. and
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RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAFL cDNAS (RAFL cDNA: RIKEN Arabidopsis Full-Length cDNA'): Seki,M., Narusaka,M., Ishida,J., Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J., Hayashizaki,Y. and Shinozaki,K.
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VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS

TITLE JOURNAL

TITLE JOURNAL REFERENCE AUTHORS

DEFINITION

RESULT 2 AY050981 LOCUS ACCESSION

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AY113986 Lhaliana putative calcium-dependent protein kinase (At1g35670) mRNA, complete cds. The Salk, Stanford, PGEC (SSP) Consortium members constructed and sequenced the PUNI (ORF) clones using the RAFL CDNAs: Yamada,K., Banh,J., Chan,M., Chang,C.H., Chang,E.D. Dale,J.M., Deng,J.M., Goldsnith,A.D., Lee,J.M., Onodera,C.S., Quach,H.L., Tang,C.C., Toriumi,M., Wu,H.C., Yamamura,Y., Yu,G., Bowser,L., Chen,H., Miranda,M., Nguyen,M., Palm,C.J., Shim,G., Kim,C., Lam,B., Lin,J., Miranda,M., Nguyen,M., Palm,C.J., Shim,P., Southwick,A., Davis,R.W., Ecker,J.R. and Theologis,A. Yamada, K. (SSP/PGEC) and Seki, M. (RIKEN GSC) contributed equally to this work. Shinozaki, K. (RIKEN GSC) and Theologis, A. (SSP/PGEC) contributed equally to this work as PIs.

Location/Qualifiers
1. 1519 1576 1627 ACATIGCIGATGCTITIGGAGITGATGGTGAAAATCIGAIGACIGACICATCATCTIC CACAATTTCTCTTTTTTTTTTTTTTTTAATTTTCGTTTTAATTTTTGAATTCTAAGG TITCIAAATITITIATCCICATAIGGATAATITITIGCTICATATAAA 1734 AY113986.1 GI:21281140 ES ource Ö SM AL SER ĕ ∞ E S œ

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                                                                                                                                                                                                                                             1 . 1488
/gene="At1g35670"
/note="contains a protein kinase PF00069 domain and
contains 4 EF hand PF00036 domains"
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llarity 99.9%; Pred. No. 0;
Conservative 0; Mismatches 2; Indels 0;
   /organism="Arabidopsis thaliana"
/db xref="taxon:3702"
/chromosome="1"
/c.cone="U10736"
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ecotype: Columbia"
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/ organism="Arabidopsis thaliana"

/ strain="Columbia"

/ db_xref="taxon:3702"

/ chromosome="4"

1. 1657

/ gene="CPR4"

/ gene="CPR4"

/ note="calcium dependent protein kinase"

/ codon start=1

/ product="calmodulin-domain protein kinase CDPK isoform 4"

/ product="calmodulin-domain protein kinase CDPK isoform 4"

/ product="calmodulin-domain protein kinase CDPK isoform 4"

/ product="calmodulin-domain protein kinase CDPK isoform 4"

/ product="calcium"
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Hrabak, E.M., Dickmann, L.J., Satterlee, J.S. and Sussman, M.R. Characterization of eight new members of the calmodulin-like domain protein kinase gene family from Arabidopsis thaliana Mol. Biol. 31 (2), 405-412 (1996)
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                                                                                                                                                                                                                                                                                                                Direct Submission
Submitted (17-JUL-1995) Estelle M. Hrabak, Horticulture, University
of Wisconsin, 1575 Linden Drive, Madison, WI 53706, USA
Location/Qualifiers
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Pred. No. 1.4e-249;
0; Mismatches 251; Indels
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Eukaryota; Viridiplantae;
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Best Local Similarity 84.1%;
Matches 1384; Conservative
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8756605
2 (bases 1 to 1657)
Hrabak, E.M.
                           .
Arabidopsis thaliana
GI:1399266
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AUTHORS
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Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
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CDPK; calmodulin-like domain protein kinase; calcium-dependent
protein kinase.
Glycine max.
Glycine max.
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Lee, J. Y., Roberts, D.M. and Harmon, A.C.

Isolation of two new (DPC isoforms (Accession Nos. U69173 and U69174) from soybean (GDPC isoforms L.) (PGR97-128)

Leant Physiol. 115, 314 (1997)

E 2 (bases 1 to 1754)

S Lee, J. Y., Yoo, B.-C. and Harmon, A.C.

Direct Submission

Lee, J. Y., Soy, B.-C. and Harmon, A.C.

Submitted (03-SEP-1996) Borany, University of Florida, 220, Be Hall, P.O. Box 118526, Gainesville, FL 32611, USA
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  1446 TGAAGCTTTTGGAGTTGA-GGACACACACCACTGCTAAATCTGATGATTCACCAAAGT
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LSSDEDAALKATDFGLSVFYKPGETFSDVVGSPYYVAPEVLCKHYGHESDVWSAGVIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YILLSGVPPPWAETDMGIFRQILRGKLDLESEPWPGISDSAKDLIRKILDRNPKRRIT
AHEVICHPWIVDDTVAPDKPLDSAVLSRLKOFSAMKKLKKVALRVIABELSEBEIGGL
KELFKMLDTDNSGTITFEELKGGLENKYGSELMESEIKDLMDAADIDNNGTIDYGEFIA
ATVHLNKLERREBULLSARSYFDKDGSGYITIEELQQACKEFGLSELNEBEJIKDIDQD
NDGQIDYKEFSAMMKGTGGAVGRRIIRNULNLGBALGLVQSEEIL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       translation="MEPKPATEPKKSSVWVLPYKTQSLQSLYTIGKKLGQGQFGTTHL"
                                                                                                                                                                                                                                                                                                                                                                                                             PLN 25-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, Asteridae, euasterids I, Solanales, Solanaceae, Solanum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
Submitted (25-NOV-2000) Nactaka Furuichi, niigata university,
Agriculture; 2-8050, Igarashi, Niigata shi, Niigata Ken 950-2181,
Japan (E-mail:nfuruiagtr.niigata-u.ac.jp,
URL:http://www.niigata-u.ac.jp, Tel:81-25-262-7520(ex.7520),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Solanum tuberosum (cultivar:Rishiri) cell suspension cDNA to mRNA, clone_lib:potato cv. Rishiri cDNA,
1223 ACTGCACTTGAATAAGATGGAAAGAGGAGAATTTGGTTGCTGCTTTCGCCTATTTTGA 1282
                                                       1283 TAAAGGTTGGTAGTGGTTACATCACCATTGACGAGCTTCAACAGGCTTGTAAGGACTTCAG 1342
                                                                                                                             1362 TCTATGTGATACACCTCTGGACGACATGATCAAGGAGATTGATCTTGACAATGACGGGAA 1421
                                                                                                                                                                 1343 CCTAGGTGATGTGCATCTGGATGATGATCAAAGAGATTGATCAAGATAATGATGGGGAG 1402
                                                                                                                                                                                                     1422 GATCGATTTCTCGGAGTTTACAGCAATGATGAGGAAAGGAGATGGA---GTTGGGAGAG 1478
                                                                                                                                                                                                                                       1403 GATTGATTATGCGGAGTTTGCAGCAATGATGAAAAGGGTGATCCAAATATGGGTAGAAG 1462
                                                                                                                                                                                                                                                                                                                                                                                                           ABOS1809

1732 bp mRNA linear PLN 25-AU Solanum tuberosum RiCDPKZ mRNA for calcium dependent protein Anase, complete cds.
ABOS1809. GI:15289759
                                                                                                                                                                                                                                                                                                               1463 CAGAACCATGAAAGGCAATTTGAACTTCAATATTGCAGATGCATTTGGAATGAAAG 1518
                                                                                                                                                                                                                                                                             1479 CAGAACCATGATGAAGAACTTGAACTTCAACATTGCTGATGCTTTTGGAGTTGATG 1534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Calcium dependent protein kinase genes from resistant and susceptible potato cultivars to Phytophthora infestans
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product="calcium dependent protein kinase"
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/tissue_type="ceall suspension"
/tissue_type="ceall suspension"
/tissue_tib="potato"
/country="Japan:Niigata,Niigata,Igarashi"
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/db_xref="GI:15289760"
/ ---"MPDKPATE
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2. .1502
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Furuichi, N. and Okuta, T.
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           DB 8; Length 1732;
46.0%; Score 803.6; DB 8; Length 71.8%; Pred. No. 2.2e-163; Live 0; Mismatches 419; Indels
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catttaaataagctggagagaggaaaaacctagtgtcggccttctcctattttgacaaa
CAGGGCCAATTCGGGGACCACCTTCGAGTGCACGCGCCGTGCGAGTGGTGGGAAGTTCGCG
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1 (bases 1 to 1768)
Holt,C.D., White,A.J., Michael,A.J. and Osborn,R.W.
Herbicide resistrant plants and methods for the production thereof
Patent: WO 0107592-A 13 01-FEB-2001;
ZENECA LIMITED (GB)
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SEIGGLKAELFKMIDTDNSGTIFPDELKDGLKRVGSELMESEIKDLMDAADIDKSGTID
YGEFTAATVHLNKLBREENLVGAFSTFDKOGGSTITLDEIQQACKDFGLDDIHLDDMI
KEIDQDNDGQIDYGEFAAMMRKGNGGIGRRTMRKTILNLRDALGLVDNGSNQVIEGYFK
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A calcium-dependent protein kinase with a regulatory domain similar
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FGTTPECTRRASGGKFACKSIPKRKLKKEDYEDVRBEIQIMHISSHANVVRIBGTY
BOSTAVHLWBELGEGEILPRIVQKGHYSERQAARLIKTIVEVVEACHSLGVMHRDLK
PENPETIIDEDAKLKAPDFGLSVFYKGESFCDVVGSPYYVAPSVIRKLYGDSSDVA
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Spermatophyta, Magnoliophyta, eudiootyledons, core eudicots,
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               1395 GATGGCAGTGGTTACATAACCCTTGATGAGATACAACAAGCTTGTAAGGACTTTGGTTTA 1454
                                                                                                       1455 GATGATATCCATATTGACGACATGATCAAGGAAATTGATCAAGATAACGATGGGCAAATA 1514
                                                                                                                                     1426 GATTICTCGGAGTTTACAGCAATGATGAGGAAAGGAGATGGAGTTGGGAGAAGCAGAACC 1485
                                                                                                                                                                  1515 GATTATGGGGAATTTGCTGCCATGATGAGAAAGGGCAATGGAGGAATTGGAAGGCGAACT 1574
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/product="unknown_protein"
/protein_id="AAB00805.1"
/db_xref="G1:1332393"
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Science 252 (5008), 951-954 (1991)
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/organism="Glycine max"
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43.3%; Score 756.4; DB 8; Length 1768;

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                                                                                                                           GITCTACCATATCAAACACCACGATTAAGAGATCATTACCTTCTGGGAAAAAAGCTAGGC 165
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                                                                                                                                                                                                                                                                226 TGCAAATCGAATCCCGAAGCGGAAAGCTCGTGTGTCGCGAGGATTACGAAGATGTATGGCGT
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                                                            Length 1693;
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                                                              Score 744.2; DB 8;
Pred. No. 1.5e-150;
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/note="37 A nucleotides"
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calcium dependent protein kinase.
Arabidopsis thaliana.
Arabidopsis thaliana.
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Nagnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Submitted (27-JAN-1995) Yan Hong, Institute of Molecular and Cell
Submitted (27-JAN-1995) Yan Hong, Institute of Molecular and Cell
Biology, National University of Singapore, 10 Kent Ridge Cresent,
Singapore, Republic of Singapore, 0511
Location/Qualifiers
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                                                                                                                                                                                                                                         TGTGATACACCTCTGGACGACATGATCAAGGAGATTGATCTTGACAATGACGGGAAGATC 1425
                                                                                                                                                                                                                                                                  GATGATATCCATATTGACGACATGATCAAGGAAATTGATCAAGATAACGATGGGCAAATA 1514
                                                                                                                                    CATTTAAATAAGCTGGAGAGAAGAGAAACCTAGTGGGCCTTCTCCTATTTTGACAAA 1394
   GATGGTTTGAAGCGAGTAGGATCTGAACTTATGGAGTCTGAAATCAAGGATCTTATGGAT 1274
                                                                                                                                                                                                                                                                                                                                      GATTATGGGGAATTTGCTGCCATGATGAAAGGGCAATGGAGGAATTGGAAGGGCGAACT
                                                            GCGGCTGATATCGACACAGTGGTACAATAGACTACGGAGAATTCCTAGCAGCAACCTTA
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/db_xref="taxon:3702"
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Arabidopsis thaliana.

Arabidopsis thaliana

Bukaryots thaliana

Bukaryots, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

I (bases I to 2036)

Hrabak, E.M., Dickmann, L.J., Satterlee, J.S. and Sussman, M.R.

Characterization of eight new members of the calmodulin-like domain protein kinase gene family from Arabidopsis thaliana

Plant Mol. Biol. 31 (2), 405-412 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ardbidopsis thaliana calmodulin-domain protein Kinase CDPK isoform (CPK) mRNA, complete cds.
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'protein id="AAB03246.1"
'db xref="GI:1399275"
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                                                                                                                                                                                                                                                                                                                                                     1366 TGTGATACACCTCTGGACGACATGATCAAGGAGATTGATCTTGACAATGACGGGAAGATC 1425
1025 GAACTGTTCAAAATGATAGACACAGATAAAAGTGGGACTATCACGTTTGAAGAGTTAAAA 1084
                                                                           1126 GCGGGTTTGAAGAGAGTCGGATCTGAACTGATGGAATCAGAATCAAGTCTCTCATGGAT 1185
                                                                                                                      1085 GATAGTATGAGACGTGTTGGGTCAGAGCTTATGGAATCAGAGATCCAAGAACTCTTGCGT 1144
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/chromosome="2"
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IVMELCAGEDLFDRIIHRGHYSERKABELTKIIVGYVBACEISLGYMRIDLKPEDFLYVH
NKDDDFSLKAIDFGLSVFRKOGIFKDVVGSPYVADFVLLKHYGFBADVWTAGVLLY
ILLSGYPPFWARATQGGTFDAVLKGYIDFDTDPWPVISDSAKDLIRKMLCSSFSBRLFA
HEVLRHPWICENGVAPDRALDPAVLSRIKOFSAMNKLKKMALKVIARSLSEBEIAGLR
MREAMDTNOSGAITPDELAGGLRRYGSTLKOFSAMNKLKKMALKVIARSLSEBEIAGLR
TIHLNKLEREBHLVAARFOYFDKOGSOYITIDELOQSGIEHGWTDVFLEDIIKEVDQDN
DGRIDYEEFVAMMQKGNAGVGRRTMKNSLNISMRDV"
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Submitrac (19-FEB-1994) Kazuo Shinozaki, Tsukuba Life Science
Submitrac (19-FEB-1994) Kazuo Shinozaki, Tsukuba Life Science
Center, The Inst. of Physical and Chemical Res., 3-1-1 Kohýádál,
Tsukuba, Ibaraki 350, Japan (E-mail:sinozaki@rtcsl.riken.go.jp,
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                                   , 1996 this sequence version replaced gi:535778 Location/Qualifiers
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Pred, No. 2.4e-142;
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1. 1858
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/gene="ATCDPK3"
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Best Local Similarity 67.8%;
Matches 987; Conservative
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/translation="MGNTCVGPSISKNGIFQSVSAAWWRSRSPDDTASTTNGESARIE
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TRTIVGVVBĀCHSLGYMHRDLKPENFIFVDQKEDSILKAIDFGLSIEPKFGDRFTDVV
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QFSAMNKLKKWALRVIĀESLSEEBIĀGLKEMFKMIDTDNSGQITFEELKEGLKRFGSN
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ADELQQACEEFGIGDVRMEEMIREADQDNDGRIDYNEFVAMMQKGNPVLGGGKKGLEH
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
                                                                                                                                                                                                                                                                                                                             Direct Submission
Submitted (25-NOV-2000) Naotaka Furuichi, niigata university,
Agriculture; 2-8050, Igarashi, Niigata shi, Niigata Ken 950-2181,
Japan (E-mailituru@agr.niigata-u.ac.jp,
URL:http://www.niigata-u.ac.jp, Tel:81-25-262-7520(ex.7520),
Pax:81-25-262-7520)
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                                                                                                                                                                                   Calcium dependent protein kinase genes from resistant susceptible potato cultivars to Phytophthora infestans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'product="calcium dependent protein kinase"
'protein id="BAB63463.1"
db_xref="GI:15289758"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /tissue type="suspension culture"
/clone lib="potato cv. Rishiri cDNA"
/country="Japan:Nilgata"
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                                                                                                                                                 Furuichi, N., Okuta, T. and Hara, N.
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Furuichi, N. and Okuta, T.
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Solanum tuberosum
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                                                                                                           708 TATGGTCCAGAAGCTGATGTGTGGACTGCTGTTATACTCTATATCTTACTAAGTGGT 767
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AGGTGGTGAGCTTTTTGATCGGATTGTTTCTAAAGGTCATTTTAGTGAGCGTGAAGCTGT
                                                                                       TGAGCTTACTAGGACTATTGTTGGGGTTGTAGAAGCTTGTCATTCTCTTGGTGTCATGCA
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REVOIMMELAGHHYVISIKARYEDAYEDIKAEMELAGHEVIIORGHYTERKAABI
TRITUGYVEACHSIGWHRDIKPENNITAVOVKBOSLIKAIDFGLSFFFKDGNFTDVV
SDPWFSISDAKDIMRRYURDPRRILTAHBYLTHPWYQNOVAPDKREDSDANLSRWK
OFSAMNKLKKMALRYIDSELSBEILAGHKERKMIDTDNGSGITFEELKOGHKRFGSN
LKESEIYDLMQAADVDNSGTIDYGEFTAATLHWYKIERQDHLFAAFCYFDKDGSGYIT
ADELQQACCEEGGIGDVRMEEMIREADQDNDGRIDYNKKIEKQDHKFFGSY
                                                                                                                                                                                                                                                                                                                                                                                                                              NTRA34155
Nicotiana tabacum mRNA for calcium-dependent protein Kinase 3 (GppA3 gene).

(GppA3 gene).

AJ44155
AJ44155.1 GI:16215470

Calcium-dependent protein kinase; cdpk3 gene.

Common tobacco.

Nicotiana tabacum
Spermarophyta; Wiridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermarophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
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/product="calcium-dependent protein kinase 3"
/protein_id="CaC8299.1"
/db_xref="GI:L6215471"
/translation="MGNTCVGPSISKNGIFQSVSAAWMRSRSPDDTASTINGESARIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Romeis,T., Ludwig,A.A., Martin,R. and Jones,J.D.
Calcium-dependent protein Kinases play an essential role in a plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
Submitted (16-AUG-2001) Romeis T., The Sainsbury Laboratory, John
Innes Centre, Norwich, Colney Lane, Norfolk, NR4 7UH, UNITED
1529
                                                        2152 GCTAGGTGGCGAAGAAGGTCTAGAGCATAGTTTCAGATTGGATTCAGAGAAGCAGT 2211
                                                                                                                   PITTICIC 1589
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   1470 TGGGAGAAGCAGAACCATGATGAAGAACTTGAACTTCAACATTGCTGATGCTTTTGGAGT
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/organism="Nicotiana tabacum"
/db_xref="taxon:4097"
374. .2110
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1501 TGTGGCTCCCGATAAGCCTCTGGATTCTGCAGTTCTGAGTAGAATGAAGCAATTTCTGC 1560
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                                                                                                               150 GGGAAAAAAGCTAGGCCAAGGCCAATTTGGAACAACCTATCTCTGCACAGAGAAATCAAC 209
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90 ACGICCIICAAACACAGIICIACCAIAICAAACACCCACGAIIAAGAGAICAIIACCIICI
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Arabidopsis thaliana.

Bukaryota; Staliana

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

(Bases I to 1967)

Hrabak, E. M., Dickmann, L. J., Satterlee, J.S. and Sussman, M.R.

Hrabak, E. M., Dickmann, L. J., Satterlee, J.S. and Sussman, M.R.

Phant, Mol. Biol. 31 (2), 405-412 (1996)
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Birect Submission
Submitted (18-UUL-1995) Estelle Hrabak, Horticulture, University of Submitted (18-UUL-1995) Estelle Hrabak, Horticulture, University of Wisconsin, 1575 Linden Drive, Madison, WI 53706, USA
Location/Qualifiers
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/codon_start=1
/product="calmodulin-domain protein kinase CDPK isoform 5"
/protein_id="AAB03245.1"
/db xref="G11399273"
/translation="MGNSCRGSFKDKLDEGDNNKPEDYSKTSTINLSSNSDHSPNAAD
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/chromosome="4"
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MISSKPAERLTAHEVLRHPWTCENGYAPDRALDPAVLSKLKGFSAWNKIKKGALKVIA
ESLSEEIAGLERNFQAMDTDNSGAITFDELKAGLKKYGSTLKOFSAWNKIKKGALKVIA
SGTIDVSEFIAATHLNKLEREEHLVAAFQYFDKAGGSTUTIDELGQACVEHGMADVD
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Chenk, R., Shinn, P., Brooks, S., Buehler, E., Chao, Q., Chio, C., Chao, S., Kim, C., Altafi, H., Bei, B., Chin, C., Chiou, J., Chol, E., Conn, L., Conway, A., Gonzalez, A., Hansen, N.,
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Arabidopsis thaliana
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Spermaryophyta; Magnoliophyta; eudicotyledons; core eudicots;
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Howing, B., Koo, T., Lam, B., Lee, J., Lenz, C., Li, J., Liu, J., Liu, J., Liu, S., Mikharsky, N., Nguyen, M., Palm, C., Pham, P., Sakano, H., Schwartz, J., Southwick, A., Thaveri, A., Toriumi, M., Vaysberg, M., Yu, G., Davis, R., Fedrspiel, N., Theologis, A. and Ecker, J. Direct Submission

Direct Submission

Submitted (28-JUN-2000) Arabidopsis thaliana Genome Center, Department of Biology, University of Pennsylvania, 38th and Hamilton Walk, Philadelphia, Philofoly 1338 bases. The On Jun 28, 2000 this sequence version replaced gis.6007863.

This submission of BAC FISO4 is shorter by 1338 bases. The Original BAC had a Thlo transposon insertion (Gb) 101829.1 [TRN101S13] from E. coli located at the junction of bases 18229 and 18230 of this submission.

Location/Qualifiers

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Arabidopsis; CDPK2; CDPK4; calcium dependent protein kinase; oilseed; disease resistance; agricultural; pathogen; crop yield; ornamental; fungicide; bactericide; nematocide; insecticide; viricide; cereal; transgenic; plant; enzyme; gene; ss.
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Arabidopsis thalia
Cucurbita pepo cal
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Arabidopsis thalia
Rice calcium depen
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| SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT:*
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                                                                                                                                                                                                                                                                                                                                                                                                     1 gatcogggtacatattcttc......tataaaagtttttgaattcc 1747
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Compugen Ltd.
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1747
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Match Length
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Score

1202.4 11183.2 756.4 688.4 652.6 629.8 597.4

Producing plant having increased disease resistance, comprises regenerating plant from a non-naturally occurring plant cell over-expressing a polynucleotide encoding a calcium dependent protein kinase polypeptide WPI; 2002-062179/08. P-PSDB; AAM48000.

Disclosure; Fig 1; 44pp; English

The invention relates to producing a plant having increased disease resistance, comprising providing a non-naturally occurring plant cell over-expressing a polynucleotide encoding a calcium dependent protein kinase (CDPK) polypeptide and regenerating a plant from the plant cell, where the CDPK polypeptide is expressed in the plant, increasing the resistance of the plant. The method is useful for a variety of agricultural and commercial purposes including improving a plant's resistance against plant pathogens, increasing crop yields, improving resistance against plant pathogens, increasing crop yields, improving crop and ornamental quality and reducing agricultural production costs. The method facilitates an effective and economical method for in-plant pathogens, increasing crop yields, improving crop and ornamical practices (e.g. application of fungicides, creatitional chemical practices (e.g. application of fungicides, contributes to the production of high quality and high yield agricultural contributes to the production of high quality and high yield agricultural contributes or graduction of high quality and high yield agricultural contributes or graduction of high quality and high yield agricultural costs and high quality and blotches that are caused by contributes or graduction of high quality and blotches that are caused by applying costs and high quality and blotches that are caused by commercial (e.g. fiber crops) purposes. The present sequence is that of Abrabidopsis thaliana CDPKZ of the invention.

Sequence 1747 BP; 516 A; 316 C; 392 G; 523 T; 0 other;

; 420 420 240 300 360 360 180 CCAAAAATGGAGACGAAAGCCAAAACCCTAGACGTCCTTCAAACACACAGTTCTACCATATCAA 120 121 ACACCACGATTAAGAGATCATTACCTTCTGGGAAAAAAGCTAGGCCAAGGCCAATTTGGA 180 Gaps GATCCGGGTACATATTCTTCTTCTTCTAAATCGAGATCGAAGAAGAACCAACAAAAAA 60 GATCCGGGTACATATICTTCTTCTTCTAAATCGAGATCGAAGAAGAACCAACAAAAAA 60 CCAAAAATGGAGGAGGAAGCCAAAACCCTAGAAGCCTTCAAACAGTTCTACCATATCAA AAGCGAAAGCTCGTGTCGCGAGGATTACGAAGATGTATGGCGTGAGATTCAGATCATG 241 AAGCGAAAGCTCGTGTCGCGAGGATTACGAAGATGTATGGCGTGAGATTCAGATCATG CATCATCTCTCTGAGCATCCAAATGTTGTTAGGATCAAAGGGACTTATGAAGATTCGGTG carcarcrereaecarecaarerrerraeeareaaeeeacrrareaaeare acaccaccartragagarcartraccrtcrgggaaaaaaccraggccaaggccaartrigga TITGITCATATTGTTATGGAGGTTTGTGAAGGTGGTGAGCTTTTTGATCGGATTGTTTCT 181 ACAACCTATCTCTGCACAGAGAATCAACCTCCGCTAATTACGCCTGCAAATCGATCCCG 100.0%; Score 1747; DB 24; Length 1747; 100.0%; Pred. No. 0; ive 0; Mismatches 0; Indels 0; Conservative Best Local Similarity Matches 1747; Conserv Query Match 181 361 121 241 301 301 361 421 원 d ò g ò 임 ò g à Op ò ò

GTCTTATCTCGTCTAAAGCAGTTTTCTCAAATGAATAAGATTAAGAAAATGGCATTACGG 1020 Graaticcigagactificagagaaagaaatiggaggicigaaggaatigiicaagaig 1080 AACAGTGGTACATTAGACTACGGAGAATTCCTAGCAGCAACCTTACACATGAACAAGATG 1260 900 900 960 600 099 999 720 720 780 780 840 840 540 480 GICTIALCHILLINAAGCAGITITCICAAATGAATAAGATTAAGAAAATGGCATTACGG GIAATTGCTGAGAGACTTTCAGAGGAAGAAATTGGAGGTCTGAAGGAATTGTTCAAGATG GTCGGATCTGAACTGGAATCAGAAATCAAGTCTCTCATGGATGCGGCTGATATCGAC GAGAGAGAGAGATTCTGGTGGCTGCATTTTCGGACTTTGACAAAGACGGAAGCGGTTAT ATCACCATCGATGAGCTTCAGTCAGCTTGCACAGAGTTTGGTCTATGTGATACACCTCTG 1321 ATCACCATCGATGAGCTTCAGTCAGCTTGCACAGAGTTTGGTCTATGTGATACACCTCTG 1441 ACAGCAATGATGAAGGAAGAAGGAGTTGGGAGAAGCAGAACCATGATGAAGAACTTG ATAGACACAGACAACAGAGGAACGATTACTTTGAAGAGCTCAAAGCGGGTTTGAAGAGA ATAGACACAGACAACAACGATTACTTTTGAAGAGCTCAAAGCGGGTTTGAAGAGA AACAGTGGTACAATAGACTACGGAGAATTCCTAGCAGCAACCTTACACATGAACAAGATG GAGAGAGAGATTCTGGTGGCTGCATTTTCGGACTTTGACAAAGACGGAAGCGGTTAT 1381 GACGACATGATCAAGGAGATTGATCTTGACAATGACGGGAAGATCGATTTCTCGGAGTTT 1381 GACGACATGATCAAGGAGATTGATCTTGACAATGACGGGAAGATCGATTTCTCGGAGTTT GATTTGATCTATAAATGCTCGAAAGGAGCCCCAAGAACGCATTTCTGCTCATGAAGCC TIGIGICACCCATGGATIGICGATGAACAAGCAGCACCAGACAAGCCICTIGAICCAGCA CTAAAGAAATGTTATGGACCTGAAATAGATGTGTGGGGGTGCTGGTGTTATCCTTACATT TTACTCAGCGGTGTTCCTCCCTTCTGGGCAGAGACTGAGTCTGGAATCTTTAGACAGATA TTGCAAGGGAAGTTAGATTTCAAATCTGACCCGTGGCCTACTATCTCAGAAGCTGCTAAA Tricchaegeaherraeantricaharcreacecereeceracratereahaecreeraha GATTTGATCTATAAAATGCTCGAAAGGAGCCCCCAAGAAACGCATTTCTGCTCATGAAGCC rrerereacecargearrereargascascascascascascererereres AAGCCAGGACAATATTTATATGACGTAGTTGGAAGTCCGTACTATGTTGCACCAGAGGTG AAAGGTCATTTTAGTGAGCGTGAAGCTGTCAAGCTTATTAAGACGATTCTTGGTGTTGTT GAGGCTTGTCATTCTCTTGGTGTTATGCATAGAGATCTCAAACCTGAGAATTTCTTGTTT GAGGCTTGTCATTCTTTGGTGTTATGCATAGGATCTCAAACCTGAGAATTTCTTGTTT CTAAAGAAATGTTATGGACCTGAAATAGATGTGTGGAGTGCTGGTGTTATCCTTACATT 1441 901 196 1021 1021 1081 1081 1141 1201 1261 1261 196 1201 1321 841 841 901 721 781 481 481 541 601 601 661 661 781 δ g à g & g ò g ò g δ g 8 qq ò g g g du ò ò ò ò ò 임 δ g ò g ò d ò g ŏ g

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Gaps

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1561 1561 1621 1621 1681 1681 1741 1741

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protection against plant pathogen, reducing or minimising the need for traditional chemical practices (e.g. application of fungicides, bactericides, nematocides, insecticides, or viricides) that are typically used bactericides, nematocides, insecticides, or viricides) that are typically browling protection against disease causing pathogens. The method contributes to the production of high quality and high yield agricultural products, e.g. fruits, ornamentals, vegetables, cereals and field crops having reduced spots, blemishes and blocches that are caused by pathogens, agricultural products with increased shelf-life and reduced handling costs and high quality and yield crops for agricultural (e.g. cereal and field crops) industrial (e.g. cilseds) and commercial (e.g. fiber crops) purposes. The present sequence is that of Abrabidopsis thaliana CDPK4 of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               855 AATGCTCGAAAGGAGCCCCAAGAAACGCATTTCTGCTCATGAAGCCTTGTGTCACCCATG 914
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          135 AGATCATTACCTTCTGGGAAAAAGCTAGGCCAAGGCCAATTTGGAACAACCTATCTCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        66 AGATCACTATCTCCTCGGCAAAAGCTAGGCCAAGGCCAATTTGGAACAACTATCTCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CACAGAGAAATCAACCTCCGCTAATTACGCCTGCAAATCGATCCCGAAGCGAAAGCTCGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TATGGAGGTTTGTGAAGGTGGTGAGCTTTTTGATCGGATTGTTTCTAAAGGTCATTTTAG
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                                                                                                                                                                                                                                                                                                                                                                                              24; Length 1657;
                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches 251; Indels
                                                                                                                                                                                                                                                                                                                                                Sequence 1657 BP; 500 A; 287 C; 384 G; 486 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                              Score 1202.4; DB 24
Pred. No. 1.6e-262;
                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 94.1%;
Matches 1384; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         735
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The present invention describes a method of producing plants which are resistant to the herbicides paraquat and diquat, involving inhibiting in the plants a calcium dependent protein kinase (CDPK) and selecting those plants which are resistant to the agrochemical of interest. This is useful in the production of crops with herbicide resistance.
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                                                                                                                                                                                Calcium dependent protein kinase; CDPK; herbicide resistance;
paraquat; diquat; crop production; ds.
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Hybridisation assay, genetic mapping, gene expression control, protein identification, signal transduction pathway, metabolic pathway, promoter, termination sequence, ss.
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73 ACGAAGCCAAAACCCTAGACGTCCTTCAAACACAGTTCTACCATATCAAACACCACGATTA 132
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99US - 0149723 . 99US - 0149929 . 99US - 0149929 . 99US - 0149929 . 99US - 0149929 . 99US - 0149929 . 99US - 0149929 . 99US - 0151086 . 99US - 0151086 . 99US - 0151080 . 99US - 0151438 . 99US - 0151438 . 99US - 0151438 . 99US - 0151438 . 99US - 0151438 . 99US - 0151438 . 99US - 0151438 . 99US - 0151438 . 99US - 0151439 . 99US - 0151438 . 99US - 0151438 . 99US - 0151438 . 99US - 0151438 . 99US - 0151438 . 99US - 0151438 . 99US - 0151438 . 99US - 0151438 . 99US - 0151438 . 99US - 0151438 . 99US - 0151438 . 99US - 0151438 . 99US - 0151438 . 99US - 0151438 . 99US - 0151438 . 99US - 0151448 . 99US - 016081 . 99US - 016081 . 99US - 016081 . 99US - 016081 . 99US - 016081 . 99US - 0161405 . 99US - 0161405 . 99US - 0161405 . 99US - 0161405 . 99US - 0161405 . 99US - 0161405 . 99US - 0161405 . 99US - 0161405 . 99US - 0161405 . 99US - 0161405 . 99US - 0161405 . 99US - 0161405 . 99US - 0161405 . 99US - 0161405 . 99US - 0161405 . 99US - 0161405 . 99US - 0161405 . 99US - 0161405 . 99US - 0161405 . 99US - 0161405 . 99US - 0161405 . 99US - 0161405 . 99US - 0161405 . 99US - 0161405 . 99US - 0161405 . 99US - 0161405 . 99US - 0161405 . 99US - 0161405 .
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                                                                                                       1452
                                                                                                                                                                                                      AGGAAAGGAGATGGAGTTGGGAGAAGCAGAACCATGATGAAGAACTTGAACTTCAACATT 1512
                                                                                                                                                                                                                                                     CAAAAGGGAAATGCTGGTGGTTGGAAGGAAGGACGATGAGAATAGTCTAAACATTAGCATG 1659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Producing herbicide resistance plants by inhibiting calcium dependent protein kinase in plants or by providing an intracellular vacuolar transporter capable of transporting agrochemical into plant vacuole
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          126
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GAGCTTCAGTCAGCTTGCACAGAGTTTGGTCTATGTGATACACCTCTGGACGACATGATC
                                              1480 GAĞCTACAACAAĞÇGTĞTGTTĞAACATĞĞCATĞĞCTĞATĞTTTTCÇTTĞAAĞACATÇATÇ
                                                                                                                                                     <u>aaagaagiigaicaaaacaaigaigaaagairgairaafirarggigagiigggagargaig</u>
                                                                                                       AAGGAGATTGATCTTGACAATGACGGGAAGATCGATTTCTCGGAGTTTACAGCAATGATG
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66.6%; Pred. No. 5.5e-138;
tive 0; Mismatches 469; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein kinase; CDPK; herbicide resistance; crop production; ds.
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                                                                                                 963 TATATGTGTGTGGAGAAGGCAACTGGGAAAGAGTATGCTTGTAAGTCTATTGCAAAGAGG 1022
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                                                                                                                                                                                                                                                                                247 AAGCTCGTGTGTCGCGAGGATTACGAAGATGTATGGCGTGAGATTCAGATCATGCATCAT 306
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The present invention describes a method of producing plants which are resistant to the herbicides paraquat and diquat, involving inhibiting in the plants a calcium dependent protein kinase (CDPK) and selecting those plants which are resistant to the agrochemical of interest. This is useful in the production of crops with herbicide resistance.
                                                                                      2103 CACGACGAGCTTCAACAAGCATGTAAAGAGTTCGGGATAGAGGATCTTCAAATGGAAGAA 2162
                                                                                                                                 1387 ATGATCAAGGAGATTGATCTTGACAATGACGGGAAGATCGATTTCTCGGAGTTTACAGCA 1446
                                                                                                                                                                   2163 ATGATGCGCGAGGTCGATCAAAACAATGACGAAGCATCGACTATAACGAGTTCGTGGCG 2222
2043 GAAGATCATCTTCTAGCAGCGTTTTCATATTTCGACAAGGAGGGAAGCGGGTTCATTACC 2102
                                             1327 ATCGATGAGCTTCAGTCAGCTTGCACAGAGTTTGGTCTATGTGATACACCTCTGGACGAC 1386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Producing herbicide resistance plants by inhibiting calcium dependent protein kinase in plants or by providing an intracellular vacuolar transporter capable of transporting agrochemical into plant vacuole
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      116 ATCAAACACCACGATTAAGAGATCATTACCTTCTGGGAAAAAAGCTAGGCCAAGGCCAAT 175
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Calcium dependent protein kinase, CDPK, herbicide resistance, paraquat, diquat, crop production, ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Vigna radiata calcium dependent protein kinase clone.
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                                                                                                                                                                                                                        1447 ATGATGAGGAAAGGAGATGGAGT 1469
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                                                                      AGTITACAGCAATGATGAAGGAAAAGGAGATGGAGTTGGGAGAAGCAGAACCATGATGAAGA
CTCTGGACGACATGATCAAGGAGATTGATCTTGACAATGACGGGAAGATCGATTTCTCGG
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                                                                                                                                              1496 ACTIGAACTICAACATIGCIGATGCTTTTGGAGTTGA 1532
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The present invention describes a method of producing plants which are resistant to the herbicides paraquat and diquat, involving inhibiting in the plants a calcium dependent protein kinase (CDFK) and selecting those plants which are resistant to the agrochemical of interest. This is useful in the production of crops with herbicide resistance.
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The present invention describes a method of producing plants which are resistant to the herbicides paraquat and diquat, involving inhibiting in the plants a calcium dependent protein Kinase (CDPK) and selecting those plants which are resistant to the agrochemical of interest. This is useful in the production of crops with herbicide resistance. 1350 1470 AAMGACGGCAAATTGACTACGCCGAATTTGTAGCCATGATGCAAGGCAGCAACGTTGGA 1910 GGGAGAAGCAGAACCATGATGAAGAACTTGAACTTCAACATTGCTGATGCTTTTGGAGTT 1530 craggergecaaacaargeaaagecagrifgaargragearraagagacgecerceaagra 1970 Producing herbicide resistance plants by inhibiting calcium dependent protein kinase in plants or by providing an intracellular vacuolar transporter capable of transporting agrochemical into plant vacuole 1670 1610 ACAGAGITTGGICTATGTGATACACCICTGGACGACATGATCAAGGAGATTGATCTTGAC TOGGACTITGACAAAGACGGAAAGCGGTTATATCACCATCGATGAGCTTCAGTTGACTTGC ggagancaranggaggartcactrgaagagarrartrgagggrigaraad AATGACGGGAAGATCGATTTCTCGGAGTTTACAGCAATGATGAGGAAAGGAGATGAGTTT TTCGGTGAGCTTAGAGAAGGTTTAAGAAGATTTGGCGCTGAATTTAAGGATACAGAGATT AAGTCTCTCATGGATGCGGCTGATATCGACAACAGTGGTACAATAGACTACGGAGAATTC getgatataárádáaadcegenen elektátaatatatotaataatatatesattateaadaattt Calcium dependent protein kinase; CDPK; herbicide resistance; paraquat; diquat; crop production; ds. Sequence 1910 BP; 560 A; 348 C; 481 G; 521 T; 0 other; calcium dependent protein kinase clone RW Osborn Claim 18; Page 38; 50pp; English. AJ, BP Michael DNA; 1910 26-JUL-2000; 2000WO-GB02876 99GB-0017642 (first entry) Holt CD, White AJ, WPI; 2001-168549/17. (ZENE) ZENECA LTD AAF74275 standard; 1975 Ipomoea batatas 1531 GATGG 1535 WO200107592-A2 potato 27-JUL-1999; 04-MAY-2001 CATTG AAF74275; Sweet 1851 1471 1911 1971 1291 1791 RESULT 10 1171 1671 1731 1351 1411 1551 1611 1231 g 6 ò g g ò g 8 ò ò g à

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Sequences AAMS2830-AAMS2842 represent novel protein kinase stress-related proteins (PKSRPs) from the moss Physcomitrella patens, and sequences ABA91069-ABA91081 represent full-length cDNAs encoding them. The cDNA
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Protein kinases, Casein kinase homologs, MAP kinases or Calcium
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Sarria-Millan R;
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sequences were obtained from expressed sequence tags (BSTS; ABA91056-ABA91068) derived from Physcomitrella patens cDNA libraries. The PKSRPS of the invantion comprise protein kinase-6 (PK-6), protein kinase-7 (PK-7), protein kinase-8 (PK-8), casein kinase-10 (PK-7), protein kinase-8 (PK-8), casein kinase-10 (PK-7), casein kinase-10 (PK-1), casein kinase-10 (PK-1), anitogen-activated protein (MAP) kinase-2 (PK-2), mitogen-activated protein (MAP) kinase-2 (PK-5), MAP kinase-1 (PK-1), and calcium-dependent protein kinase-1 (PK-1), and calcium-dependent protein kinase-1 (PK-1), and calcium-dependent protein kinase-1 (PK-1), and calcium-dependent protein kinase-2 (PK-1), and calcium-dependent protein kinase-1 (PK-1), and calcium-dependent protein kinase-1 (PK-1), and calcium-dependent protein kinase-1 (PK-1), and calcium-dependent protein kinase-1 (PK-1), and calcium-dependent protein kinase-1 (PK-1), and calcium-dependent protein kinase-1 (PK-1), and calcium-dependent protein stresses such as salinity, drought tolerance to environmental stresses such as salinity, drought and sendent protein acids may be used to generate the proper participal patens professed plants generated can be monocots or dicots and are especially maize, wheat, rye, oat, tritcale, rice, cotton, rapessed, cassava, sunflower, tagetes, leguminous plants (e.g., soybean, peanut, vicia species, alfalfa), solanaceous plants salix species, oil palm, coconut, perennial grasses and forage crops. The propertion artuctural studies and as markers for specific regions of
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                                                                                                                                                             The present invention describes a method of producing plants which are resistant to the herbicides paraquat and diquat, involving inhibiting in the plants a calcium dependent protein Kinase (CDK) and selecting those plants which are resistant to the agrochemical of interest. This is useful in the production of crops with herbicide resistance.
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                                                                                                                                                                                                                                                                                                                                                          Score 522.8; DB 22; Length 1791;
Pred. No. 1.2e-108;
0; Mismatches 527; Indels 9;
                                                                                                                                                                                                                                                                                                            Sequence 1791 BP; 554 A; 286 C; 448 G; 503 T; 0 other;
                                                                                             Claim 18; Page 34-35; 50pp; English
                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 61.8%;
Matches 868; Conservative
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                                                                                                                               Griccrictagaargaagdagrircagagdaargaldaacaagcricaagdrirgdacriraag
                                                                                                                                                                                                              GTAATTGCTGAGAGACTTTCAGAGGAAGAAATTGGAGGTCTGAAGGAATTGTTCAAGATG
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                                                                       GTCTTATCTCGTCTAAAGCAGTTTTTCTCAAATGAATAAGATTAAGAAAATGGCATTACGG
protein kinase; CDPK; herbicide resistance; crop production; ds.
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Claim 18; Page 43-44; 50pp; English.

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The present invention describes a method of producing plants which are resistant to the herbicides paraquat and diquat, involving inhibiting in the plants a calcium dependent protein Kinase (CDPK) and selecting those plants which are resistant to the agrachemical of interest. This is useful in the production of crops with herbicide resistance.
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                                                                                                                                                       Sequence 2363 BP; 718 A; 435 C; 542 G; 668 T; 0 other
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Best Local Similarity 60.3
Matches 898; Conservative
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GGCTAAGAGATGGTGAAGCAT---CAGACAAGCCAATAGACAGTGCTGTTCTCCTCAGGA
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                                                        TAAAGCAGTTTTCTCAAATGAATAAGATTAAGAAAATGGCATTACGGGTAATTGCTGAGA
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paraquat; diquat; crop production; ds.
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The present invention describes a method of producing plants which are resistant to the herbicides paraguat and diquat, involving inhibiting in the plants a calcium dependent protein Kinase (CDFK) and selecting those plants which are resistant to the agrachemical of interest. This is useful in the production of crops with herbicide resistance.
protein kinase in plants or by providing an intracellular vacuolar transporter capable of transporting agrochemical into plant vacuole
                                                                             Claim 18; Page 36-37; 50pp; English
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Sequence 2436 BP; 738 A; 435 C; 515 G; 747 T; 1 other;

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ence 2430 BF; /30 AF; %35 C; 313 G; /47 F; 1 Other; atch 29.8%; Score 520.2; DB 22; Length 2436; cal Similarity 64.5%; Pred. No. 5.2e-108; 793; Conservative 0; Mismatches 433; Indels 3; Gaps	actitigggaaaaaggtaggccaaggccatitiggaacaactaictigcacagaga 202 	aatcaacciccggtaattacgcctgcaaatcgatcccgaagcgaaagcggagcgg 262 	AGGATTACGAAGATGTATGGCGTGAGATTCAGATCATGCATCATCTCTGAGCATCCAA 322 	AIGTTGTTAGGATCAAAGGGACTTATGAAGATTCGGTGTTTGTT			TIATGCATAGAGATCTCAAACCTGAGAATTTCTTGTTTGATAGTCCTAAAGATGATGCTA 562 		ACGTAGTIGGAAGTCCGTACTATGTTGCACCAGAGGTGCTAAAGAAATGTTATGGACCTG 682 	AAATAGAIGIGIGGAGIGCTGGIGTTAICCICTACAFITTACTCAGGGGGTGTICCTCCCT 742 	TCTGGGCAGAGACTGAGTCTGGAATCTTTAGACAGATATTGCAAGGGAAGTTAGATTTCA 802 	AATCTGACCGTGGCCTACTATCTCAGAAGCTGCTAAAGATTTGATCTATAAAATGCTCG 862 	AAAGAAGCCCCAAGAAACGCATTTCTGCTCATGAAGCCTTGTGTCACCCATGGATTGTCG 922	AIGAAGAAGGACCAGAAGCTCTTGATCCAGCAGTCTTATCTCGTCTAAAGCAGT 982
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1043 AGGAAGAAATTGGAGGTCTGAAGGAATTGTTCAAGATGATAGACACAGACAACAGCGGAA 1102
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983 TITCTCAAATGAATAAGATTAAGAAAATGGCATTACGGGTAATTGCTGAGAGACTTTCAG 1042
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APPLICANT: Dawson, John L.
APPLICANT: Dawson, John L.
APPLICANT: Dunder, Erik M.
APPLICANT: Pace, Gary M.
TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE NUMBER OF SEQUENCES: 94
CORRESPONDENCE ADDRESS:
ADDRESSEE: CIRA-COTT.
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SOFTWARE: PACENTIN Release #1.0, Version #1.30B
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/951,715A
FILING DATE: 25-SEP-1992
CLASSIFICATION NUMBER: US/07/72,027
APPLICATION NUMBER: 00 70/772,027
APPLICATION NUMBER: 07/772,027
ATTONNEY/AGENT INFORMATION:
NAME: SPENTING NUMBER: 32,943
REGISTRATION NUMBER: 32,943
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US-09-056-52-52
US-09-1359-161-4
US-08-611-097-3
US-08-611-097-3
US-08-557-0066-37
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US-08-818-253-3
US-08-818-252-3
US-08-818-252-3
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Patent No. 5625136
GENERAL INFORMATION:
APPLICANT: Koziel, Michael G.
APPLICANT: Lewis, Kelly S.
APPLICANT: Lewis, Kelly S.
APPLICANT: Kramer, Vance C.
APPLICANT: Warren, Gregory W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 10532
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Crossland, Lyle D.
Wright, Martha S.
Marlin, Ellis J.
Launis, Karen L.
Rothstein, Steven J.
Bowman, Cindy G.
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                                                                                 February 13, 2003, 17:50:37; Search time 75 Seconds (without alignments) 7143.524 Million cell updates/sec
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(/GGTZ_6/ptodata/2/ina/5A_COMB.seq:*
//GGTZ_6/ptodata/2/ina/5B_COMB.seq:*
//GGTZ_6/ptodata/2/ina/6A_COMB.seq:*
//GGTZ_6/ptodata/2/ina/6A_COMB.seq:*
//GGTZ_6/ptodata/2/ina/PGTUS_COMB.seq:*
//GGTZ_6/ptodata/2/ina/PGTUS_COMB.seq:*
//GGTZ_6/ptodata/2/ina/PGTUS_COMB.seq:*
                 GenCore version 5.1.3
(c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                      441362 segs, 153338381 residues
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                                                                                                                                                                                                                                                                                                                                                     Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                       - nucleic search, using sw model
                                                                                                                                                                                                              IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                              seq length: 0
seq length: 200000000
                                                                                                                                                       US-09-848-806-2
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Match Length
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                                                                                                                                                                                                                                                                                                                                                                                                             Database
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1021 ACAĞÇĞĞĞTACATTACTAAAĞAAĞAĞÇTTGAĞCACĞCCİTGAAĞĞĞCAAĞĞĞTİĞTATĞ 1080
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APPLICANT: Wright, Martha S.
APPLICANT: Wright, Martha S.
APPLICANT: Wright, Martha S.
APPLICANT: Rothstein, Seeven J.
APPLICANT: Rowman, Cindy G.
APPLICANT: Bowman, Cindy G.
APPLICANT: Dunder, Erik M.
APPLICANT: Pace, Gary M.
APPLICANT: Pace, Gary M.
APPLICANT: Suttle, Janet L.
APPLICANT: Suttle, Janet L.
APPLICANT: Strike, Janet L.
APPLICANT: Strike, Janet L.
APPLICANT: Strike, Janet L.
APPLICANT: STRIFFTIC DNA SEQUENCE HAVING ENHUTTLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHUTTLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE OF MUMBER OF SEQUENCES: 94
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ADDRESSEE: No. 5859336artis Corporation
STREET: Patent & Trademark Dept., 520 White Plains
STREET: Rd., POB 2005
CITY: Tarrytown
STATE: New York
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ZIP: 10591-9005
COMPUTER READABLE PORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: TIM PC COMPATIBLE
COMPUTER: PATENTING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/459,448A
FILLING DATE: 02-UUN-1995
CLASSIFICATION: 800
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24.6%; Score 429.8; DB 1; Length 1349;
Best Local Similarity 60.3%; Pred. No. 1.46-99;
Matches 729; Conservative 0; Mismatches 477; Indels 3;
                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 1349 base pairs
TYPE: nucleic acid
STRANDENNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
FEATURE:
                                                      INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: CDS
LOCATION: 3..1226
OTHER INFORMATION: /
OTHER INFORMATION: 6
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TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENH
TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE
TITLE OF SEQUENCES: 94
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6018104artis Corporation
STREET: Patent & Trademark Dept., 520 White Plains
STREET: Rd., POB 2005
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Merlin, Bllis J.
Launis Karen L.
Rothstein, Steven J.
Bowman, Cindy G.
Dawson, John L.
Dunder, Erik M.
Pace, Gary M.
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Dessi, Nalini M.
Lewis, Kelly S.
Kramer, Vance C.
Warren, Gregory W.
Evola, Stephen V.
Crossland, Lyle D.
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APPLICATION NUMBER: US 07/951,715
FILING DATE: 25-SEP-1992
PRIOR APPLICATION DATA: US 07/772,027
FILING DATE: 04-OCT-1991
ATTORNEY,ACBNT INFORMATION:
NAME: PACE, GATY M.
REGISTATION NUMBER: 40403
REFERENCE/DOCKET NUMBER: CGC 1577/CIP/DIV4
TELECHONE: (919)541.8689
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 1349 base pairs
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STRANDENNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
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APPLICANT: Koziel, Michael G. APPLICANT: Desai, Nalini M.
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Desai, Nalini M.
Lewis, Kelly S.
Kramer, Vance C.
Warren, Gregory W.
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Wright, Martha S.
Merlin, Ellis J.
Launis, Karen L.
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US-08-459-504B-20
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CITY: Tarrytown
STATE: New York
CUUNTRY: USA
ZIP: 10591-9005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OFBRATUG SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATCHIN DATA:
APPLICATION NUMBER: US/08/459,595A
FLING DATE: 02-JUN-1995
CLASSIFICATION NUMBER: US/08/459,595A
FLING DATE: 25-JUN-1995
FLING DATE: 25-SEP-1992
RICHATION NUMBER: US 07/951,715
FILING DATE: 25-SEP-1992
RICHATION NUMBER: US 07/72,027
FILING DATE: 04-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAMM: DATE: GAT' M.
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REGISTRATION NUMBER: 40403
REFERENCE/DOCKET NUMBER: CGC 1577/CIF/DIV3
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (919)541-8582
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TYPE: nucleic acid
STRANDEDNESS: single
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NAMBKEY: CDS
LOCATION: 3. 1226
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MOLECULE TYPE: CI
HYPOTHETICAL: NO
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                                                                 APPLICANT: Bowman, Cindy G.
APPLICANT: Dawson, John L.
APPLICANT: Dawson, John L.
APPLICANT: Dunder, Erik M.
APPLICANT: Pace, Garry M.
APPLICANT: Suttie, Janet L.
TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE NUMBER OF SEQUENCES: 94
CORRESPONDENCES: 94
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
APPLICATION DATA:
RIGHT APPLICATION NUMBER: US/g8/459,504B
FILING DATE:
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APPLICATION NUMBER: US 08/459,595
FILING DATE: 02-07197195
APPLICATION NUMBER: US 07/951,715
FILING DATE: 25-SEP-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/72,027
FILING DATE: 04-0CT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Meigs J. Timochy
REGISTRATION NUMBER: 38.24
REGISTRATION NUMBER: 38.24
REGISTRATION NUMBER: 38.24
TELECHOME: (919) 541-8689
TELECHOME: (919) 541-8689
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STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
                       Rothstein, Steven J
Bowman, Cindy G.
Dawson, John L.
Dunder, Erik M.
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INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
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Matches 729; Conservative
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FEATURE:
NAWE/KEY: CDS
LOCATION: 3.1226
OTHER INFORMATION:
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STRANDEDNESS: singl
TOPOLOGY: linear
MOLECULE TYPE: cDNA
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STATE: NO
COUNTRY:
ZIP: 2771
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     410 GGATIGTTTCTAAAGGTCATTTTAGTGAGCGTGAAGCTGTCAAGCTTATTAAGACGATTC 469
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                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: No. 6121014artis Agribusiness Biotechnology Research, Inc.
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            350 AAGATTCGGTGTTTGTTCATATTGTATGGAGGTTTGTGAAGGTGGTGAGCTTTTTGATC 409
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                                                                                                                                                                                                                                                                                                                        INVENTION: METHOD FOR PRODUCING A PLANT-OPTIMIZED NUCLEIC ACID CODING SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: S-18805/P1/CGC1577/CIP/DIV6
TELECOMMINICATION: (910)541-8587
TELEPPAK: (910)541-8689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/459,444A
FILING DATE: 02-Jun-1995
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/951,715
FILING DATE: 25-SEP-1992
APPLICATION NUMBER: US 07/772,027
FILING DATE: 04-OCT-1991
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SEQUENCE DESCRIPTION: SEQ ID NO: 20:
                                                                                 APPLICANT: Koziel, Michael G.
Desai, Nalini M.
Lewis, Kelly S.
Kramer, Vance C.
Warren, Gregory W.
Evola, Stephen V.
Crossland, Lyle D.
Wiright, Marcha S.
Marlin, Ellis J.
Launis, Karen L.
               Sequence 0, Application US/08459444A Patent No. 6121014 GENERAL INFORMATION:
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LENGTH: 1349 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
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NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241

REFERENCE/DOCKET NUMBER: 5-18805H

TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-6587

TELEPHONE: (919)541-6587

TELEPHONE: (919)541-6587

TELEPAX: (919)541-6587

TELEPAX: (919)641-6587

TELEPAX: (919)641-6587

TELEPAX: (919)641-6587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESSE:
No. 6320100artis Agribusiness Biotechnology Research, Inc.
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: NC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24.6%; Score 429.8; DB 4; Length 1349; 60.3%; Pred. No. 1.4e-99; tive 0; Mismatches 477; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Launis, Karen L.
TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED INSECTICIDAL ACTIVITY IN MAIZE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATE:
APPLICATION NUMBER: US 08/459,595
FILING DATE: 02-0UN-1995
APPLICATION NUMBER: US 07/951,715
FILING DATE: 25-SEP-1992
APPLICATION NUMBER: US 07/772,027
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 27709
COMPUTER READABLE FORM:
MEDLUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Ven
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/547, 422
FILING DATE: 11.Apr-2000
CLASSIFICATION: 
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LOCATION: 3..1226
SEQUENCE DESCRIPTION: SEQ ID NO: 20:
                                                                                                                     LENGTH: 1349 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
FEATURE:
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       COUNTRY:
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Matches 729;
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FEATURE:
NAME/KEY:
LOCATION:
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                                                                                                            1141 ATTATTCAGAGTTTGTGGCGATGATGAGGGACGGCTGGTGGTGCGAGCCAATGAACA 1200
1081 ACGCCGATAAAATCAAAGACATCATCTCCGATGCCGACTCTGACAATGATGGAAGGATAG 1140
                                                              1427 ATTICICGGAGITIACAGCAATGATGAGGAAAGGAGAIGGAGITGGGAGAAGCAGAACCA 1486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Adams, Karen L.
APPLICANT: Sothsein, Steven J.
APPLICANT: Bowman, Cindy G.
APPLICANT: Bowman, Cindy G.
APPLICANT: Dawson, John L.
APPLICANT: Dawson, John L.
APPLICANT: Dawson, John L.
APPLICANT: Dawson, John L.
APPLICANT: Dawson, John L.
APPLICANT: Dawson, John L.
APPLICANT: Dawson, John L.
APPLICANT: Dawson, John L.
TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE
NUMBER OF SECUENCES: 94
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 585936artis Corporation
STREET: Patent & Trademark Dept., 520 White Plains
STREET: Patent & Trademark Dept., 520 White Plains
STREET: Wew York
COUNTRY: USA
COUNTRY: USA
ZIP: 10591-9005
COUNTRY: DEADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Patent In Release #1.0, Version #1.30
CORRENT APPLICATION DATA:
APPLICATION NUMBER: US 07/951,715
FILING DATE: 25-582-1992
PRIOR APPLICATION NUMBER: US 07/772,027
FILING DATE: 04-CT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Pace, Gary M.
REFERENCE/DOCKET NUMBER: GC 1577/CIP/DIV4
TELECOMMUNICATION NUMBER: GC 1577/CIP/DIV4
TELECOMMUNICATION NUMBER: GC 1577/CIP/DIV4
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
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                                                                                                                                                                                                                                                                                                                                                         US-08-459-448A-26
; Sequence 26, Application US/08459448A
; Patent No 5859336
; GENERAL INFORMATION:
APPLICANT: Koziel, Michael G.
APPLICANT: Lewis, Kelly S.
APPLICANT: Lewis, Kelly S.
APPLICANT: Kramer, Vance C.
APPLICANT: Ewis, Kelly S.
APPLICANT: Ewis, Kelly S.
APPLICANT: Ewis, Kelly S.
APPLICANT: Evola, Stephen V.
APPLICANT: Crossland, Lyle D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kramer, Vance C.
Warren, Gregory W.
Evola, Stephen V.
Crossland, Lyle D.
Wright, Martha S.
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NO
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Launis, Karen L.
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TYPE: nucleic acid
STRANDEDNESS: single
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 4162 base pairs
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TYPE: PYT
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/function= "pollen-specific promoter region"
/evidence= EXPERIMENTAL
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Best Local Similarity 59.8%; Pred. No. 9.4e-46;
Matches 365; Conservative 0; Mismatches 245; Indels
PEATURE:

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NAME/KEX: intron
LOCATION: 3499..3713
FEATURE:
NAME/KEX: exon
LOCATION: 3714..3811
FEATURE:
NAME/KEX: promoter
LOCATION: 1..1477
IDENTIFICATION METHOD: e:
COTHER INFORMATION: /func
JOTHER INFORMATION: /func
COTHER INFORMATION: /func
JC-08-459-448A-26
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LOCATION:
1997 CTGTGCGCGGGGGGGGGCTCTTCGACCGCATCATCGCCCGGGGCCAGTACACGGAGCGC 2056
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                                                                        442 GAAGCTGTCAAGCTTATTAAGACGATTCTTGGTGTTGTTGAGGCTTGTCATTCTCTTGGT 501
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APPLICANT: Crossland, Lyle D.
APPLICANT: Wright, Martha S.
APPLICANT: Martin, Elis J.
APPLICANT: Launis, Karen L.
APPLICANT: Launis, Karen L.
APPLICANT: Launis, Karen L.
APPLICANT: Launis, Steven J.
APPLICANT: Launis, Steven J.
APPLICANT: Launis, Steven J.
APPLICANT: Dawson, John L.
APPLICANT: Dawson, John L.
APPLICANT: Dawson, John L.
APPLICANT: Dawson, John L.
APPLICANT: Statis, Jamet L.
APPLICANT: Statis, Jamet L.
APPLICANT: Statis, Jamet L.
APPLICANT: Statis, Jamet L.
APPLICANT: Statis, Jamet L.
APPLICANT: Statis, Jamet L.
APPLICANT: No. 6018104artis Corporation
STREET: No. 6018104artis Corporation
STREET: Ratent & Trademark Dept., 520 White Plains
STREET: Ratent & Trademark Dept., 520 White Plains
STREET: No. 6018104artis Corporation
STREET: No. 6018104artis Corporation
STREET: No. 6018104artis Corporation
STREET: Ratent & Trademark Dept., 520 White Plains
STREET: Now York
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Is Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,595A
FILING DATE: 20-201-1092
PRIOR APPLICATION NUMBER: US 07/951,715
FILING DATE: 25-55EP-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 26, Application US/08459595A Patent No. 6018104 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Koziel, Michael G. Desai, Nalini M. Lewis, Kelly B. Kramer, Vance C. Warren, Gregory W. Evola, Stephen V. Crossland, Lyle D. Wright, Martha S. Merlin, Ellis J. Launis, Karen L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2357 TTCTGGGCAG 2366
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US-08-459-595A-26
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OTHER INFORMATION: /function= "pollen-specific promoter region"
OTHER INFORMATION: /evidence= EXPERIMENTAL
US-08-459-595A-26
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APPLICATION NUMBER: US 07/772,027
FILING DATE: 04-007-1991
ATCONEY/AGENT INFORMATION:
NAME: Pace, Gary M.
REGISTRATION NUMBER: 40403
REGISTRATION NUMBER: GGC 1577/CIP/DIV3
REFERENCE/COCKET NUMBER: GC 1577/CIP/DIV3
TELEFRAN: (919)541-8689
INFORMATION FOR SEQ ID NO: 26: SEQUENCE CHARACTERISTICS:
LENGTH: 416.2 base pairs
TYPE: nucleic acid
STRANDENESS: single
                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc_feature

LOCATION: 1418..1427

FORHER INFORMATION: /note= "start of mRNA"

FORHER: NAME/KEY: exon
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LOCATION: 3714..3811
FEBATURE:
NAME/KEY: promoter
LOCATION: 1..1477
IDENTIFICATION METHOD: experimental
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MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
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TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
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STATE: NC
COUNTRY: US
ZIP: 27709
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                                                                                                                                                                                                                                                                                                                                                                                                    382 GITIGIGAAGGIGGIGAGCITITIGATCGGATIGITICIAAAGGICATITITAGIGAGCGT 441
          142 TACCITCTGGGAAAAAGCTAGGCCAAGGCCAATTTGGAACAACCTATCTCTGCACAGAG 201
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                                                                                                                                                                                                                                                                      SQUENCE 26, Application US/08459504B

SQUENCE 26, Application US/08459504B

SAPLICANT: Koazel, Michael G. APPLICANT: Koazel, Michael G. APPLICANT: Lewis, Kelly S. APPLICANT: Lewis, Kelly S. APPLICANT: Lewis, Kelly S. APPLICANT: Warren, Vance C. APPLICANT: Warren, Stephen V. APPLICANT: Wright, Martha S. APPLICANT: Merlin, Elis J. APPLICANT: Merlin, Elis J. APPLICANT: Merlin, Elis J. APPLICANT: Merlin, Elis J. APPLICANT: Merlin, Elis J. APPLICANT: Bowman, Cindy G. APPLICANT: Bowman, Cindy G. APPLICANT: Bowman, Cindy G. APPLICANT: Suttie, Eik M. APPLICANT: Suttie, Eik M. APPLICANT: Suttie, Janet L. TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING WUMBER OF SUFURNING AND INSECTICIDAL ACTIVITY IN MAIZE WUMBER OF SEGUENCES PARMANCED
                                                                                                                                    202 AAATCAACCTCCGCTAATTACGCCTGCAAATCGATCCCGAAGCGAAAGCTCGTGTGTCGC
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ADDRESSEE: No. 607515sartis Corporation STREET: 3054 Cornwallis Road CITY: Research Triangle Park
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US-08-459-504B-26
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COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

MEDIUM TYPE: Floppy disk

CORPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

PRIOR APPLICATION NUMBER: US 08/459,595

FILING DATE: 02-UN-1995

APPLICATION NUMBER: US 07/951,715

FILING DATE: 25-SEP-1992

PRIOR APPLICATION NUMBER: US 07/772,027

FILING DATE: 04-OCT-1991

ATTORNEY/AGENT INFORMATION:

NAME: Meight, J. Timchy

REGISTRATION NUMBER: GGL577/CIP/DIV

REGISTRATION NUMBER: GGL577/CIP/DIV

TELEPAX: (919)541-8689

INPORMATION POR SEQ ID NO: 26:

SEQUENCE CHRAACTERISTICS:

LENGTH: 4162 base pairs

TYPE: nucleic caid

STRANDENBESS: single

TOPOLOGY: linear

TOPOLOGY: linear

TOPOLOGY: linear
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LOCATION: 1418<sup>7</sup>.1427
OTHER INFORMATION: /note= "start of mRNA"
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PRIOR APPLICATION DATE: US 07/951,715
FILING DATE: 25-SEP-1992
APPLICATION NUMBER: US 07/772,027
FILING DATE: 04-OCT--1991
ATTORNEY/AGENT INFORMATION:
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MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
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STRANDEDNESS: single
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42 TTCTGGGCAG 7b.

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US-08-459-444-26
Sequence.26, Application US/0845944A
PAPLICANT: Koziel, Michael G.
Deash, Nalini M.
Lewis, Kelly S.
Kramer, Vance C.
Warren, Gregory W.
Evola, Stephen V.
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Best Local Similarity 59.8
Matches 365; Conservative
       intron
3499..3713
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3714..3811
NAME/KEY:
LOCATION:
FEATURE:
NAME/KEY:
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US-08-459-504B-26
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NUMBER OF SEQUENCES: 94

CORRESPONDENCE ADDRESS:
ADDRESSE: No. 6121014artis Agribusiness Biotechnology Research, Inc.
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: NC
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKEN NUMBER: S-18805/P1/CGC1577/CIP/DIV6
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8587
TELEPAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                 COMPUTER READBLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRINT APPLICATION NUMBER: US/08/459,444A
PILING DATE: 02-Jun-1995
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
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LOCATION: 14187.1427
OTHER INFORMATION: /note= "start of mRNA"
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Launis, Karen L.
TITLE OF INVENTION: SYNTHEIC DNA SEQUENCE HAVING ENHANCED
INVENTION: INSECTICIDAL ACTIVITY IN MAIZE
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LOCATION: 1418 .. 1427
CTHER INFORMATION: /note= "start of mRNA"
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INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHRACTERISTICS:
LENGTH: 4162 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              442 GAAGGTGTCAAGGTTATTAAGACGATTCTTGGTGTTGTTGAGGCTTGTCATTCTTGGT 501
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                                                                                                                                                                             Query March
12.5%; Score 218; DB 3; Length 4162;
Best Local Similarity 59.8%; Pred. No. 9.4e-46;
Matches 365; Conservative 0; Mismatches 245; Indels
                                                                                           NAME/KEY: exon
LOCATION: 3714..3811
SEQUENCE DESCRIPTION: SEQ ID NO: 26:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NESULA 1-22-26

Sequence 26, Application US/09547422

Sequence 26, Application US/09547422

Patent No. 6320100

GENERAL INFORMATION:

Desai, Nalini M.

Lewis, Kelly S.

Kramer, Vance C.

Warren, Gregory W.

EVOLA, Stephen V.

CCOSSland, Lyle D.

Wright, Martha S.

Merlin, Ellis J.
                                         intron
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     3399..3498
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NAME/KEY:
LOCATION:
       LOCATION:
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NUMBER OF SEQUENCES: 94
CORRESPONDENCE ADDRESS:
ADDRESSE: NO. 6320100artis Agribusiness Biotechnology Research, Inc. STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
                                                                                                                                                                                                       COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDLUM TYRE: Floppy disk
COMPUTER: IN PC compatible
COMPUTER: IN PC compatible
COMPUTER: IN PC COMPACE
SOFFWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/547,422
FILING DATE: 11-APP-200

PRIOR APPLICATION NUMBER: US 08/459,595
FILING DATE: 02-JUN-1995
APPLICATION NUMBER: US 07/951,715
FILING DATE: 04-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Madigs, J. Timochy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: S-18805H
TELECOMMUNICATION NUMBER: S-18805H
TELECOMMUNICATION NUMBER: S-18805H
TELECOMMUNICATION NUMBER: S-18805H
TELECOMMUNICATION NUMBER: S-18805H
TELECOMMUNICATION NUMBER: S-18805H
TELECOMMUNICATION NUMBER: S-18805H
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APPLICANT: Warren, Gregory W.
APPLICANT: Evola, Stephen V.
APPLICANT: Crosland Lyle D.
APPLICANT: Wright, Martha S.
APPLICANT: Wright, Martha S.
APPLICANT: Merlin, Ellis J.
APPLICANT: Merlin, Ellis J.
APPLICANT: Bowman, Cindy G.
APPLICANT: Bowman, Cindy G.
APPLICANT: Bowman, Cindy G.
APPLICANT: Dunder, Erik M.
APPLICANT: Duttie, Jane E.
APPLICANT: Suttie, Janet L.
APPLICANT: Suttie, Janet L.
APPLICANT: Suttie, Janet L.
APPLICANT: Suttie, Janet L.
APPLICANT: Suttie, Janet L.
APPLICANT: SUTTIE OF INVENTION: SYNTHERIC DNA SEQUENCE HAVING ENHANCED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER:
FLING DATE: 25-SEP-1992
CLASSIFICATION NUMBER: W6/07/951,715A
FILING DATE: 25-SEP-1992
CLASSIFICATION NUMBER: W60
PRIOR APPLICATION NUMBER: W6 07/772,027
ATTON NUMBER: W6 07/772,027
FILING DATE: 04-0CT-1991
ATTON NUMBER: 32,943
REGISTRATION NUMBER: 32,943
REGISTRATION NUMBER: 32,943
REGISTRATION NUMBER: 32,943
REGISTRATION NUMBER: 32,943
REGISTRATION NUMBER: 32,943
REGISTRATION NUMBER: 32,943
REGISTRATION NUMBER: S-18805/A/CGC 1577/CIP
TELECOMMULICATION INFORMATION:
TELEPHONE: (919) 541-8615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
NAME/KEY: misc feature
LOCATION: 1416...1425
OTHER INFORMATION: /note= "start of mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 7 Skyline Drive
CITY: Hawthorne
STATE: New York
COUNTY: USA
ZIP: 10532
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 94
CORRESSONDENCE ADDRESS.
ADDRESSEE: CIBA-GRIGY Corporation
STREET: 7 Skyline Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (919)541-8669
INFORMATION FOR SEQ ID NO: 26: SEQUENCE CHARACTER.STICS:
LENGTH: 4165 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
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                                                                                                                                                                                                                                                                                                                                                             Query Match
12.5%; Score 218; DB 4; Length 4162;
Best Local Similarity 59.8%; Pred. No. 9.4e-46;
Matches 365; Conservative 0; Mismatches 245; Indels
                                                                                                                                                                                                                                              NAME/KEY: exon
LOCATION: 3714..3811
SEQUENCE DESCRIPTION: SEQ ID NO: 26:
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Sequence 26, Application US/07951715A

Patent No. 5623136

GENERAL INFORMATION:
APPLICANT: Roziel, Malini M.
APPLICANT: Lewis, Kelly S.
APPLICANT: Lewis, Kelly S.
APPLICANT: Kramer, Vance C.
                                                                                                    exon
3399..3498
                                                                                                                                                                           intron
3499..3713
                                intron
3305..3398
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LOCATION:
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Patent No. 6262345
GENERAL INFORMATION:
APPLICANT: Allen, Steve
APPLICANT: Lee, Jian Ming
TITLE OF INVENTION: Plant Protein Kinases
FILE REFERENCE: BB-1171
CURRENT APPLICATION NUMBER: US/09/347,801
CURRENT FILING DATE: 1999-07-02
EARLIER APPLICATION NUMBER: 60/092,438
EARLIER FILING DATE: UNJY 10, 1998
NUMBER OF SEQ ID NOS: 23
SOFTWARE: Microsoft Office 97
SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 2374
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Matches 365; Conservative 0; Mismatches 245; Indels
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US-09-347-801-3
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NAME/KEY: 11

LOCATION: 3

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NAME/KEY: 62

LOCATION: 32

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                                                                                                                                                                                                                    Length 2374;
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                                                                                                                                                                                                                           Query Match 10.9%; Score 189.6; DB 4;
Best Local Similarity 53.8%; Pred. No. 1.2e-38;
Matches 440; Conservative 0; Mismatches 369;
; TYPE: DNA
; ORGANISM: Oryza sativa
US-09-347-801-3
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793 TIAGATITICAAATCIGACCCGTGGCCTACTATCTCAGAAGCTGCTAAAAGATTTGATCTAT 852
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271 AGCGAGGGGGATGCAGCTCGTATAGTACGTCAGGTTCTATCGGGTATAAATTATGCAT 330
                                                                                                                                                                                                                                                                  613 TATITATATGACGTAGTTGGAAGTCCGTACTATGTTGCACCAGAGGTGCTAAAGAAATGT 672
                                                                                                                                                                                                                                                                                                              451 AAAATGAAGGATAAAATCGGGACCGCGTACTACATTGCCCCTGAGGTGCTGCACGGAACA 510
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                                                                                                                       331 CGTAATAAATAGTTCATAGAGTTTAAAGCCAGAGAATTTATTATTAGAGAATAAAAAA 390
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                                                                                                                                                                     GATGATGCTAAGGCTACCGATTTTGGTTTGTCTGTCTTCTATAAGCCAGGACAA
                                                                         493 TCTCTTGGTGTTATGCATAGAGATCTCAAACCTGAGAATTTCTTGTTTGATAGTCCTAAA
                                                                                                                                                                                                                391 AAAGATGCAAATATACGAATTATTGATTTTGGGTTATCTACACATTTTGAGCCCCAAAAA
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COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
APPLICATION DATA:
APPLICATION NUMBER: US/08/338,057
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APPLICANT: Tomley, Fiona M.
APPLICANT: Dunn, Paul P. J.
APPLICANT: Bunstead, Janene M.
APPLICANT: Vermeulen, Arno N.
TITLE OF INVENTION: Coccidiosis poultry vaccine
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Organon Teknika Corporation
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APPLICATION NUMBER: EP 93.309078.9
FILING DATE: 12-NOV-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Application US/08338057
Patent No. 5795741
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REGISTRATION NUMBER: 34,409
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 258-5200
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Rockville
STATE: Maryland
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Organ
STREET: 1330 Pic
CITY: Rockville
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    373 GITAIGGAGGIITGTGAAGGIGGIGAGCITITITGAICGGAITGITICIAAAGGICALTIT 432
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9.4%; Score 165; DB 1; Length 14
Best Local Similarity 54.5%; Pred. No. 1.6e-32;
Matches 330; Conservative 0; Mismatches 275; Indels
                                                                                                                                                                                                                                                                                                                             LESSEE - ANDRESS:
STREET: 1300 Piccard Drive, Suite 206
CITY: Nockville
STATE: Maryland
COUNTRY: U.S.A.
ZIP: 20850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LIBRARY: sporozoite cDNA cloned in Lambda ZAPII
CLONE: Em70-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/464,164 FILING DATE: June 2, 1995 CLASSIFICATION: 435 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                     APPLICANT: Tomley, Fiona M.
APPLICANT: Dunn, Paul B. J.
APPLICANT: Bunn, Paul B. J.
APPLICANT: Wermeulen, Arno N.
TITLE OF INVENTION: Coccidiosis poultry vaccine
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                      1048 GAAATTGGAGGTCTGAAGGAATTGTTCAAGATGATAGA 1085
                                                                                 1620 GAACTTTGTATCTCAAACTGCAGTTTAAACTGCTCGA 1657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN: Houghton
DEVELOPMENTAL STAGE: sporozoite
                                                                                                                                                                          US-08-464-164-1
Sequence 1, Application US/08464164
Patent No. 5614195
GENERAL INFORMATION:
APPLICANT: Tomley, Fiona M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: GORMLey, Mary E.
REGISTRATION NUMBER: 34,405
TELECOMMUNICATION INFORMATION
TELEPHONE: (301) 258-5200
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: CDNA to MRNA HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Eimeria maxima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ANTI-SENSE: NO FRAGMENT TYPE: C-terminal ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 1400 base pairs
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EDNESS: double
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MEDIUM TYPE: Floppy
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STRANDEDNESS:
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9.4%; Score 165; DB 1; Length 1400;
Best Local Similarity 54.5%; Pred. No. 1.6e-32;
Matches 330; Conservative 0; Mismatches 275; Indels
                                                                                                                                                                                                                                                                                                                                  ANTI-SENSE: NO
FRAGMENT TYPE: C-terminal
ORIGINAL SOURCE:
ORIGINAL SOURCE:
ORGANISM: Eineria maxima
STRAIN: Houghton
DEVELOPMENTAL STAGE: sporozoite
IMMEDIATE SOURCE:
LIBRARY: sporozoite cDNA cloned in Lambda ZAPII
CLONE: Em70-1
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Search completed: February 13, 2003, 21:06:29 Job time : 103 secs
LENGTH: 1400 base pairs
TYPE: nucleic acid
STRANDENESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA tO MRNA
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           913 TGGAT 917
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February 13, 2003, 19:10:42; Search time 99 Seconds (without alignments) 8987.762 Million cell updates/sec
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1. /ggn2_6/ptodata/1/pubpna/USO7_PUBCOMB.seq:*
2. /ggn2_6/ptodata/1/pubpna/PCTNM_VEW_PUB.seq:*
3. /ggn2_6/ptodata/1/pubpna/PCO6_PUBCOMB.seq:*
4. /ggn2_6/ptodata/1/pubpna/USO6_PUBCOMB.seq:*
5. /ggn2_6/ptodata/1/pubpna/USO6_PUBCOMB.seq:*
6. /ggn2_6/ptodata/1/pubpna/USO8_WEW_PUB.seq:*
7. /ggn2_6/ptodata/1/pubpna/USO8_WEW_PUB.seq:*
8. /ggn2_6/ptodata/1/pubpna/USO8_WEW_PUB.seq:*
10. /ggn2_6/ptodata/1/pubpna/USO9_PUBCOMB.seq:*
11. /ggn2_6/ptodata/1/pubpna/USO9_PUBCOMB.seq:*
12. /ggn2_6/ptodata/1/pubpna/USO9_PUBCOMB.seq:*
13. /ggn2_6/ptodata/1/pubpna/USO9_PUBCOMB.seq:*
13. /ggn2_6/ptodata/1/pubpna/USO9_PUBCOMB.seq:*
13. /ggn2_6/ptodata/1/pubpna/USO0_PUBCOMB.seq:*
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14. /ggn2_6/ptodata/1/pubpna/USO0_PUBCOMB.seq:*
GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                        OM nucleic - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Result No.	Score	Query Match	Length	DB	ID	Description
-	1484 8	, c	4441	10	TIS-09-938-8428-704	and 104 and almos
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m	712.6	40.8	1635	σ	US-09-938-842A-2344	Sequence 2344, Ap
4	643.4	36.8	1833	σ	US-09-938-842A-2334	2334,
S	531.8	30.4	2230	10	US-09-828-313-26	Sequence 26, Appl
9	507.8	29.1	1638	φ	US-09-938-842A-1859	Seguence 1859, Ap
7	448.2	25.7	455	10	US-09-770-444-571	Sequence 571, App
80	444.6	25.4	1602	σ	US-09-938-842A-2304	Sequence 2304, Ap
σv	277.8	15.9	1387	10	US-09-828-313-13	Sequence 13, Appl
0 10	227.4	13.0	955	10	US-09-770-445-326	Sequence 326, App
11	221.6	12.7	2253	10	US-09-828-313-25	Sequence 25, Appl
12	200.6	11.5	1800	σ	US-09-938-842A-1063	063
13	193	11.0	718	σ	US-09-938-842A-3678	Sequence 3678, Ap
14	189.6	10.9	2374	10	US-09-854-731-3	Sequence 3, Appli
15	168	9.6	413	10	US-09-878-574-3809	Sequence 3809, Ap
16	159.6	9.1	1372	10	US-09-817-181-1	
17	155	8 6.8	267	10	US-09-923-876-331	Sequence 331, App
18	145.6	8.3	1074	σ	US-10-024-036B-3	Sequence 3, Appli
19	145.6	8.3	1578	10	US-09-835-788A-6	Sequence 6, Appli

927727 952	Sequence 4541, Ap Sequence 162, App Sequence 2190, App Sequence 267, App Sequence 6, Appli Sequence 8, Appli Sequence 10, Appli Sequence 5432, Ap Sequence 5432, App Sequence 502, App Sequence 502, App
US-10-024-036B-1 US-09-878-574-13205 US-10-116-332-1 US-10-001-835-82 US-09-214-093B-3865 US-09-294-093B-3865 US-09-35-464-4 US-10-096-960-1 US-10-044-090-27 US-09-796-692-7777 US-09-796-692-7777 US-09-978-574-7818 US-09-928-299-200	999
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Sequence 704, Application US/09938842A

Patent No. US20020160378A1

Patent No. US20020160378A1

APPLICANT: Harper, Jeff

APPLICANT: Kreps, Joel

APPLICANT: Wang, Xun

APPLICANT: AL, Tong

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FILE REPERENCE: SCRIP1300-3

CURRENT PILING DATE: 2001-08-24

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PRIOR FILING DATE: 2001-01-16

PRIOR FILING DATE: 2001-01-16

PRIOR FILING DATE: 2001-01-16

PRIOR FILING DATE: 2001-01-16

PRIOR FILING DATE: 2001-06-22

NUMBER OF SEQ ID NOS: 5379

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                                   CATATICITATICGAGGITTGTGAAGGTGGTGGTGTTTTTTGATCGGATTGTTTTAAAGGT
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; Patent No. US20020160378A1
; General No. US20020160378A1
; General No. US20020160378A1
; General No. US200201603A1
; APPLICANT: Marge, Joef
APPLICANT: Warge, Joef
APPLICANT: Warge, Warn
APPLICANT: Warge, Warn
APPLICANT: Warge, Warn
APPLICANT: Warge, Warn
APPLICANT: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS
TILLE OF INVENTION: STRESS-REGULATED GENES OF USE
FILE REFERENCE: SCR.P1300-3
; CURRENT APPLICATION NUMBER: US/09/938,842A
; FILE REPLICATION NUMBER: US 60/227,866
; FILNG DATE: 2000-08-24
; FILNG DATE: 2001-01-16
; PRIOR FILING DATE: 2001-01-16
; PRIOR PLING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; SEQ ID NO 786
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42.6%; Score 744.2; DB 9;
Best Local Similarity 70.0%; Pred. No. 3.4e-158;
Matches 1001; Conservative 0; Mismatches 428;
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US-09-938-842A-2344
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RESULT 3

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APPLICANT: ALGO, UNCONTROLLATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING TITLE OF INVENTION: SAME, AND METHODS OF USE FILE REFERENCE: SCRIP1300-3 CURRENT PEPELGATION NUMBER: US/09/938,842A CURRENT PILING DATE: 2001-08-24 PRIOR APPLICATION NUMBER: US 60/227,866 PRIOR FILING DATE: 2001-08-24 PRIOR FILING DATE: 2001-01-16 PRIOR FILING DATE: 2001-01-16 PRIOR FILING DATE: 2001-01-16 PRIOR FILING DATE: 2001-01-16 PRIOR FILING DATE: 2001-01-16 PRIOR FILING DATE: 2001-01-05-25 NUMBER OF SEQ ID NOS: 5379
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68.3%; Pred. No. 4.6e-151;
tive 0; Mismatches 459;
Sequence 2344, Application US/09938842A Patent No. US20020160378A1
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; ORGANISM: Arabidopsis thaliana
US-09-938-842A-2344
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Patent No. US20020160378A1
GENERAL INFORMATION:
APPLICANT: Harper, Jeff
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PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 2334
; LENGTH: 1833
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Sequence 26, Application US/09828313
SEQUENCE 26, Application US/09828313
SEPLICANT: COSTA e SILVA, OSWALDO DA APPLICANT: COSTA e SILVA, NOCHA VAN APPLICANT: THIELEN, NOCHA VAN APPLICANT: THIELEN, NOCHA VAN APPLICANT: SARRIA-MILLAN, RODRIGO
TITLE OF INVENTION: PROTEIN KINASE STRESS-RELATED PROTEINS AND METHODS OF TITLE OF INVENTION: USE IN PLANTS
TITLE OF INVENTION: USE IN PLANTS
TITLE OF INVENTION NUMBER: 05/095828,313
CURRENT PRICATION NUMBER: 05/196,001
PRIOR APPLICATION NUMBER: 05/196,001
PRIOR PILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 128
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 26
LENGTH: 2230
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; ORGANISM: Physcomitrella patens
US-09-828-313-26
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Sequence 1859, Application US/09938842A

Patent No. US20020160378A1

GENERAL INFORMATION:

APPLICANT: Harper, Jeff

APPLICANT: Kreps, Joe1

APPLICANT: Wang, Xun

APPLICANT: Wang, Xun

APPLICANT: Wang, Xun

APPLICANT: Wang, Xun

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APPLICANT: Wang, Xun

APPLICANT: Wang, Xun

APPLICANT: Wang, Xun

APPLICANT: Zhu, Tong

TITLE OF INVENTION: SAME, AND METHODS OF USE

TITLE OF INVENTION: SAME, AND METHODS OF USE

TITLE OF INVENTION NUMBER: US 60/227, 866

PRIOR FILING DATE: 2001-08-24

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PRIOR FILING DATE: 2001-06-22

NUMBER OF SEQ ID NOS: 5379

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                                                                                                                                                                                                                                                                                             GTCAGCTTGCACAGAGTTTGGTCTATGTGATAC---ACCTCTGGACGACATGATCAAGGA 1397
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               GATTGATCTTGACAATGACGGGAAGATCGATTTCTCGGAGTTTACAGCAATGATGAGGAA 1457
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             1682 CAACGAGITCATAICGGCAACAATGCACAIGAACAAGAAGAAGAAGAAGAAGATCACCTITG 1741
                                                                                                                                                                                                         Gecaecarrcarecarrredacacedacaaradedegrarareacearedaedaetrea 1801
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          176 readceacaaaracarerraderegreaarraderegadeegaarregaareacrrace 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             236 TCTGTACTGATCGTGAAACCCACGAAGCTTTAGCTTGCAAATCGATTTAAAGCGAAAGC 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        251 TCGTGTGTCGCGAGGATTACGAAGATGTATGGCGTGAGATTCAGATCATGCATCATCTCT 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           296 TICGAACAGCTGTCGATATCGAAGACGTTCGTCGTGAGGTAGCGATTATGTCTACTTTAC 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         356 cicadcarccaaacciaciraacciraagciraciariarcaccaraaccacacciccarc 415
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1458 AGGAGATGGAGTTGGGAGAAGCAGAACCATGATGAAGAA 1496
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; ORGANISM: Arabidopsis thaliana
US-09-938-842A-1859
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-938-842A-1859
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APPLICANT: Kreps, Jost
APPLICANT: Kreps, Jost
APPLICANT: Kreps, Jost
APPLICANT: Wang, Xun
APPLICANT: Wang, Xun
APPLICANT: Wang, Xun
APPLICANT: Buy, Town
TITLE OF INVENTION: SAME, AND METHODS OF USE
FILE REPRENCE: SCRIP1300.3
CURRENT APPLICATION NUMBER: US 60/227, 866
PRIOR APPLICATION NUMBER: US 60/227, 866
PRIOR FILING DATE: 2000-08-24
PRIOR FILING DATE: 2000-08-24
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-01-06-22
NUMBER OF SEQ ID NOS: 5379
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   229 ATCAAAACGGGCGAGAAGTATCCGTGCAAGTCTATATCAAACAAGAAGATTAGAACAGCT 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         289 gradananadaganginagadagangingaganangadaganangcanagacacca 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      322 AAIGITGITAGGATCAAAGGGACTTATGAAGATTCGGTGTTTGTTCATATTGTTATGGAG 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AATATCGTGTCGCTGAAGGATGCCTTTGAGGATGATGATGCAGTGCATATAGTTATGGAG 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               409 rigigidadedadereacterritearcedarrerrectachedectriniaracreaded 468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     469 ecreciecrecasigaigaadacraricirgaagirgricadaraieccaraagcardaa 528
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     562 AAGCITAAGGCTACCGAITTIGGTTTGTCTGTCTTCTATAAGCCAGGACAATATTTATAT 621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    649 GAGATIGITGGAAGICCITATIACAIGGCACCAGAGGIACITAGGCGAAATIACGGACCI 708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              682 GAAATAGATGTGTGGAGTGCTGGTGTTATCCTCTACATTTTACTCAGCGGTGTTCCTCCC 741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   142 TACCTICTGGGAAAAAGCTAGGCCAAGGCCAATTTGGAACAACCTATCTCTGCACAGAG 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                202 AAATCAACCTCCGCTAATTACGCCTGCAAATCGATCCCGAAGCGAAAGCTCGTGTGGTCGC 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              622 GACGTAGTTGGAAGTCCGTACTATGTTGCACCAGAGGTGCTAAAGAAATGTTATGGACCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         382 GITTGIGAAGGIGGIGAGCITTTIGAICGGAITGITTICTAAAGGICATTITAGIGAGGG
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                                                      421 daagardgarrrcrcggagrrracagdaargarga 455
                                                                                                                                                                                                  Sequence 2304, Application US/09938842A Patent No. US/20020160378A1 GENERAL INFORMATION: APPLICANT: Harper, Jeff APPLICANT: Kreps, Joel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA ORGANISM: Arabidopsis thaliana
                                                                                                                                                                               US-09-938-842A-2304
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GCTCAAAGCGGGTTTGAAGAGAGTCGGATCTGAACTGATGGAATCAGAAATCAAGTCTCT 1178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CATGGATGCGGCTGATATCGACAACAGTGGTACAATAGACTACGGAGAATTCCTAGCAGC 1238
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TGACAAAGACGGGAAGCGGTTATATATCACCATCGATGAGCTTCAGCTTGCACAAAAGTT 1358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                999 GATTAAGAAAATGGCATTACGGGTAATTGCTGAGAGACTTTCAGAGGAAGAAATTGGAGG 1058
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AACCTTACACATGAACAAGATGGAGAGAGAGAATCTGGTGGCTGCATTTTCGTACTT 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 TCTGAAGGAATTGTTCAAGATGATAGACACAGACAGCGGAACGATTACTTTTGAAGA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GCTCAAAGCGGGTTTGAAGAGAGTCGGATCTGAACTGATGGAATCAGAATCAAAGTCTT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CATGGATGCGGCTGATATCGACAACAGTGGTACAATAGACTACGGAGAATTCCTAGCAGC 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 GATTAAGAAAATGGCATTACGGGTAATTGCTGAGAGACTTTCAGAGGAAGAAATTGGAGG 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Hurban, Parrick
TITLE OF INVENTION: Expressed Sequences of Arabidopsis
TITLE OF INVENTION: Expressed Sequences of Arabidopsis
TITLE OF INVENTION: Expressed Sequences of Arabidopsis
FILE REPERBORS: 2027 (PARA-016PRV)
CURRENT FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: 60/178,502
PRIOR APPLICATION NUMBER: 60/178,502
PRIOR FILING DATE: 2000-01-27
NUMBER OF SEQ ID NOS: 999
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 455
Sequence 571, Application US/09770444 Patent No. US20020023280A1
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CTHER INFORMATION: n = A,T,C or US-09-770-444-571
                                                                                                                                                                                                                                                                                                  Page, Amy Abraham V. Ledford, Brooke L. Woessner, Jeffrey P. Haas, William David Garcia, Carlos A. Kricker, Maja Slader, Ted Davis, Keith R. Allen, Keith Hoffman, Neil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Arabidopsis thaliana
                                                                                                               An, Yong-Qiang
Hamilton, Carol M.
Price, Jennifer L.
Raines, Tracy M.
                                                                                                                                                                                                                                            Yu, Yang
Rameaka, Joshua G.
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; Sequence 25, Application US/09828313; Patent No. US20020059662A1; GENERAL INFORMATION:
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ORGANISM: Physcomitrella patens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 128
SOFTWARE: Patentin Ver. 2.1
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502; Conserv
                                                                                                                                                            RESULT 11
US-09-828-313-25
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Best Local S
Matches 502
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAGTCTCTCATGGATGCGGCTGATATCGACAACAGTGGTACAATAGACTACGGAGAATTC 1230
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                                                                                                                              Davis, Keith R.

Davis, Keith R.

APPLICANT: Allen, Keith Neil
APPLICANT: Hoffman, Neil
APPLICANT: Hoffman, Neil
APPLICANT: Hoffman, Patrick
IITLE OF INVENTION: Expressed Sequences of Arabidopsis
IITLE OF INVENTION: Lalian
FILE REFERENCE: 2023US (PARA-012PRV)
CURRENT FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: US 60/178,472
PRIOR FILING DATE: 2000-01-27
NUMBER OF SEQ ID NOS: 999
SOFTWARE: FastSEQ for Wind~
SEQ ID NO 326
LENGTH: 955
LENGTH: 955
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                                                                                                                       Matthew, Abraham V.
Ledford, Brooke L.
Woessner, Jeffrey P.
Haas, William David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
, ORGANISM: Arabidopsis thaliana
US-09-770-445-326
An, Yong-Qiang
Hamilton, Carol M.
Price, Jennifer L.
Raines, Tracy M.
                                                                                       Joshua G.
                                                                                                             Page, Amy
                                                                         fu, Yang
                                                                                          Катеака,
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APPLICANT: CSTR & SILVA, OSWALDO DA
APPLICANT: HANS J.
APPLICANT: THIELEN, NOCHA VAN
APPLICANT: CHEN, ROUTIAN, ROBRIGO
APPLICANT: CHEN, ROUTIAN, ROBRIGO
APPLICANT: SARATA-MILLAN, ROBRIGO
APPLICANT: SARATA-MILLAN, ROBRIGO
TITLE OF INVENTION: PROTEIN KINASE STRESS-RELATED PROTEINS AND METHODS OF
TITLE OF INVENTION: USE IN PLANTS
FILE REFERENCE: 16313-0032
CURRENT FILING DATE: 2001-04-06
PRIOR PRILIAG DATE: 2000-04-07
PRIOR PRILIAG DATE: 2000-04-07
PRIOR PRILIAG DATE: 2000-04-07
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                                                                                             1351 ACAGAGTTTGGTCTATGTGATACACCT---CTGGACGACATGATCAAGGAGATTGATCTT 1407
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478 CAACACTTTGATAAAGACAACAGGGGGCACATAAACTAGAGATGAGTTGGAAAGTGCCATG 419
                                                                                                                                                                            235 ATCCCGAAGCCAAAGCTCGTGTGTCGCGAGGATTACGAAGATGTATGGCGTGAGATTCAG 294
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646 GAGGACAATGCCAACGTITACATCGTTATGGAGTTATGTGGAGGTGGTGAACTTCTTGAC 705
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US-09-938-842A-3678
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pacent No. US20020160378A1

GENERAL INFORMATION:

APPLICANT: Harper, Jeff

APPLICANT: Wang, Xun

APPLICANT: Wang, Xun

APPLICANT: Wang, Xun

APPLICANT: Wang, Xun

APPLICANT: Wang, Xun

APPLICANT: Wang, Xun

APPLICANT: Wang, Xun

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APPLICANT: Wang, Xun

APPLICANT: Wang, Xun

APPLICANT: Wang, Xun

APPLICANT: Wang, Xun

APPLICANT: SAME, AND METHODS OF USE

CURRENT APPLICATION NUMBER: US 60/227, 866

PRIOR FILING DATE: 2001-08-24

PRIOR FILING DATE: 2001-01-16

PRIOR FILING DATE: 2001-01-16

PRIOR FILING DATE: 2001-01-16

PRIOR FILING DATE: 2001-06-22

NUMBER OF SEQ ID NOS: 5379

LENGTH: 1800
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                                                                                                                                                                                                                                                              1224 GCACAAGCTTTAACTCATCCATGCATTCGAAGTAACAACG-----TGAAGATACCTCTG 1277
                                                                                                                                                                                                                                                                                                      GATCCAGCAGTCTTATCTCGTCTAAAGCAGTTTTCTCAAATGAATAAGATTAAGAAAATG 1011
                                                                                                                                                                                                                                                                                                                                            1278 GATATCTTAGTGTACAGACTTGTGAGGAATTATCTTCGTGCATCATCCATGAGAAAGGCT 1337
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    1044 ACGIACATITIGITATGIGGIAGICGATTTIGGGCGCGGGACCGAGCGGGCATTITT 1103
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                                                                   AGACAGATATTGCAAGGGAAGTTAGATTTCAAATCTGACCCGTGGCCTACTATCTCAGAA
                                                                                                                                               GCTGCTAAAGATTTGATCTATAAATGCTCGAAAGGAGCCCCCAAGAAACGCATTTCTGCT
                                                                                                                                                                                   GAAGCCAAGGATTTCGTGAAGCGTCTCCTGAATAAGGATATGCGGAAACGCATGACTGCT
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11.5%; Score 200.6; DB 9; Length:
Best Local Similarity 52.4%; Pred. No. 9.1e-36;
Matches 490; Conservative 0; Mismatches 439; Indels
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| Sequence 3678, Application US/09938842A | Sequence 3678, Application US/09938842A | Sequence 3678, Application US/09938842A | Sequence 3678, Application | Sequence 3678, Applicant | Sequence 3678, Applicant | Sequence 3788, Joel | Applicant | Mang, Xun | Applicant | Mang, Xun | Applicant | Mang, Xun | Applicant | Mang, Xun | Applicant | Mang, Xun | Applicant | Mang, Xun | Applicant | Mang, Xun | Applicant | Same, And methods of USE | TITLE OF INVENTION: SAME, AND METHODS OF USE | TITLE FERRENCE: SCRIPIONO 3 | TITLE OF INVENTION | SAME, AND METHODS OF USE | CURRENT Application NUMBER: US 60/227,866 | PRIOR APPLICATION NUMBER: US 60/227,866 | PRIOR APPLICATION NUMBER: US 60/227,866 | PRIOR APPLICATION NUMBER: US 60/264,647 | PRIOR FILING DATE: 2001-01-16 |
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Query Match
Best Local Similarity 63.2
Matches 258; Conservative
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                                                                                                                                                                                    Query Match
11.0%; Score 193; DB 9; Length 718;
Best Local Similarity 100.0%; Pred. No. 2.8e-34;
Matches 193; Conservative 0; Mismatches 0; Indels
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53.8%; Pred. No. 2.7e-33;
Live 0; Mismatches 369; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 3, Application US/09854731
Patent No. US20020120949A1
GENERAL INFORMATION:
APPLICANT: Allen, Steve
APPLICANT: Lee, Jian Ming
TITLE OF INVENTION: Plant Protein Kinases
FILE REPERENCE: BB-1171
CURRENT APPLICATION NUMBER: 60/09/854,731
CURRENT FILING DATE: 2001-05-14
PRIOR APPLICATION NUMBER: 60/092,438
PRIOR FILING DATE: July 10, 1998
NUMBER OF SEQ ID NOS: 23
SEQ ID NO 3: 580
      60/300,111
                                                                                                                                                                                                                                                                   1555 CTCATCATTCTTCCACAATTTCTGTTTTTT
PRIOR APPLICATION NUMBER: US 60/31
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379
SEQ ID NO 3678
LENGTH: 718
TYPE: DDA
ORGANISM: Arabidopsis thaliana
US-09-938-842A-3678
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Best Local Similarity 53.88
Matches 440; Conservative
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CORGANISM: Oryza sativa
US-09-854-731-3
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APPLICANT: Byrum, Joseph R.
APPLICANT: Byrum, Joseph R.
APPLICANT: Byrum, Thomas J.
APPLICANT: La Rosa, Thomas J.
APPLICANT: La Rosa, Thomas J.
APPLICANT: La Rosa, Thomas J.
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21 (15401)B
CURRENT APPLICATION NUMBER: US/09/878,574
CURRENT FILING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: 09/333,535
PRIOR FILING DATE: 1999-06-14
NUMBER OF SEQ ID NOS: 15775
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CTHER INFORMATION: Clone ID: LIB3028-005-Q1-B1-E8
US-09-878-574-3809
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US-09-878-574-3809
i Sequence 3809, Application US/09878574
Patent No. US20020110548A1
GENERAL INFORMATION:
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1074 CAAGATGATAGACACAGAGAGGACGATTACTTTTGAAGAGCTCAAGGGGTTT 1133
244 TGCCAACATGGACACTGACAATAGTGGCACTATCACCTATGAGAATTAAAGACTGGCTT 303
                                                                                                                                             954 TCCAGCAGTCTTATCTCGTCTAAAGCAGTTTTCTCAAATGAATAAGATTAAGAAAAATGGC 1013
                                               1014 ATTACGGGTAATTGCTGAGAGACCTTCAGAGGAAGAAATTGGAGGTCTGAAGGAATTGTT 1073
               1194 TATCGACAACAGTGGTACAATAGACTACGGAGAATTCCTAGCAGCAAC 1241
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Submitted (25-ARR-2002) Maize Mapping Project, University of Submitted (25-ARR-2002) Missouri, Columbia, MO 65211, USA
Location/Qualifiers
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/db_xref="MaizeDB:630671"
/db_xref="taxon:4577"
/clone="CL1905_1"
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Zea mays CL1905_1 mRNA sequence.
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Unpublished (2002)
2 (bases 1 to 2380)
Coe,E.C.
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AUTHORS
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                      GenCore version 5.1.3
(c) 1993 - 2003 Compugen Ltd.
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/note="this sequence is part of a project of EST
assemblies resulting from the application of public
contigs to seed DuPont contigs; this resource was
assembled by DuPont as part of a collaboration for the
overgo addressing of BACs in conjunction with the Maize
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Seki, M., Narusaka, M., Ishida, J., Kamiya, A., Satou, M., Nakajima, M., Soki, M., Narusaka, M., Carninci, P., Kawai, J., Itoh, M., Ishii, Y., Arakawa, T., Shbata, K., Shinagawa, A., Muramatsu, M., Hayashizaki, Y. and Shinozaki, K.
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Arabidopsis thaliana
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta, Viridiplantae, eudicotyledons; core eudicots;
Spermatophyta; Magnoliophyta; eudicotyledons; Arabidopsis.
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1064 AGGAATTGTTCAAGATGATAGACACAGACAACAGCGGAACGATTACTTTTGAAGAGCTCA 1123
                                                                                                                                                                                                                                                                                                                                                                                                                              1429 GTCCACTGGATCCAGCTGTCTTATCTCGCATTAAGCAATTCTCTGCAATGAATAAGTTGA 1488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Large scale analysis of Arabidopsis full-length cDNA (2002b)
Unpublished (2002)
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                                                                                                                                                                                                                  1489 AGADADIGGTTTACGAGTDATAGCTGAGAGCCTATCAGAAGAGGADATTGCGGGGTTGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1669 ATGCAGCTGATATTGACAACAGTGGAACAATTGACTACATAGAATTCATTGCTGCAACTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1244 TACACATGAACAAGATGGAGAGAGAGAGATTCTGGTGGCTGCATTTTCGGACTTTGACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TATGTGATACACCTCTGGACGACATGATCAAGGAGATTGATCTTGACAATGACGGGAAGA
                                                                                                               AGAAAATGGCATTACGGGTAATTGCTGAGAACTTTCAGAGGAAGAAATTGGAGGTCTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CCATGATGAAGAACTTGAACTTCAACATTGCTGATG 1519
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AV825282
AV825282.1 GI:19867342
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KEYWORDS
SOURCE
ORGANISM
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Anotes this sequence is part of a project of EST assemblies resulting from the application of public contigs to seed DuPont contigs, this resource was assembled by DuPont as part of a collaboration for the overgo addressing of BACs in conjunction with the Maize
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   998 redreardeadereradeadeadeadeadeadererreaaceadeareareadeadeadeadea 1057
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   491 ATTCTCTTGGTGTTATGCATAGAGATCTCAAACCTGAGAATTTCTTGTTTGATAGTCCTA 550
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         131 TAAGAGATCATTACCTTCTGGGAAAAAGCTAGGCCAAGGCCAATTTGGAACAACCTATC 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   251 TCGTGTGGCGAGGATTACGAAGATGTATGGCGTGAGATTCAGATCATGCATCATCTCT 310
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                                                                                                                                                                                                                                                                                         /organism="Zea mays"
/db xref="MaizeDB:630315"
/db xref="000014577"
/clone="Cil46 1"
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Maize Mapping Project/DuPont Consensus Sequences for Design
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             191 TCTGCACAGAGAAATCAACCTCCGCTAATTACGCCTGCAAATCGATCCCGAAGCGAAAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                371 TIGITAIGGAGGITIGTGAAGGIGGIGGIGAGCTITITGAICGGAITGITICTAAAGGICATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                431 TTAGTGAGCGTGAAGCTGTCAAGCTTATTAAGACGATTCTTGGTGTTGTTGAGGCTTGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1058 ACACCGAGAAGGCAGCCGAGCTCGCCGCGTCATCGTCGCGCGTCGTGGAGGCGTGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1238 AAATTTTCACCGACGTCGTGGGCAGCCCTTACTACTACGGGCGCCGGAGGTACTGAAGAAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   671 GITAIGGACCIGAAATAGAIGIGIGGAGIGCIGGIGITAICCICIACAITITACICAGCG
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Submitted (25-APR-2002) Maize Mapping Project, University
Missouri, Columbia, MO 65211, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Match 30.0%; Score 523.6; DB 11; Length 2566; Local Similarity 60.2%; Pred. No. 5.4e-86; Loservative 0; Mismatches 528; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             249 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             420 E
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680 c 777
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2 (bases 1 to 2566)
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                                                                                                                      Coe, E.C.
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Best Local S:
Matches 799
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ORIGIN
                                                                                                                   AUTHORS
TITLE
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TITLE
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1 (bases 1 to 2566)
Hainey, C.F., Dolan, M., Miao, G.H., Vogel, J.M., Whitsitt, M.S., Arthur, L.W., Hanafey, M., Morgante, M. and Tingey, S.V.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             138 GATTAAGAGATCATTACCTTCTGGGAAAAAGCTAGGCCAAGGCCAATTTGGAACAACT 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATCTCTGCACAGAGAAATCAACCTCCGCTAATTACGCCTGCAAATCGATCCCGAAGCGAA 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      rerereagearceaardricinadearcaaaceachtareaacarriceachtrichte 377
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                68 IGGAGACGAAGCCAAACCCTAGACGICCTICAAACAGAGTICTACCATAICAAACACCAC 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             regagaceaaeccaaeccraeeccricercaaecacacricraceararcaaecacac 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         128 GATTAAGAGATCATTACCTTCTGGGAAAAAGCTAGGCCAAGGCCAATTTGGAACAAGCT 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Arcretecacagagaarcaaccredecraarracecerecaaarcaarcegaagegaa 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AGCTCGTGTGTCGCCGAGGATTACGAAGATGTATGGCGTGAGATTCAGATCATGCATCATC 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      258 AGCTCGTGTGTCGCGAGGATTACGAAGATGTATGGCGTGAGATTCAGATCATGCATCATT 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18 GITTATCATCTTCTTCTTCAAATCGAGATCGAGGAGGAGCAACAAAAAAA 77
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0
                                                                                                                                                                                                                                                                                                                                                                                      32.2%; Score 563.4; DB 10; Length 591;
.larity 98.8%; Pred. No. 4.7e-93;
Conservative 0; Mismatches 7; Indels 0;
                                                                                                                                                                                                                                         Sali; subjected
hr)"
                                                                                                                                                                                                                                                                                                      1 others
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                   1...591
/organism="Arabidopsis thaliana"
/db_xref="taxon:3702"
/clone="RAFLO7-07-KIG"
/clone="RAFLO7"
/dev etage="rosette plants"
/lab_host="DH10B"
/note="Site 1: BamH1; Site_2: Sal
cold-treated (1, 2, 5, 10, 24 hr)
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Hainey, C.F., Dolan, M., Miao, G.H., Vogel, J.M., Whitsitt, M.S., Arthur, L.W., Hanafey, M., Morgante, M. and Tingey, S.V. Maize Mapping Project/DuPont Consensus Sequences for Design C Unpublished (2002)
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29.0%; Score 505.8; DB 11; Length 2298;
Best Local Similarity 61.8%; Pred. No. 9.9e-83;
Matches 817; Conservative 0; Mismatches 502; Indels 3;
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Medicago truncatula
bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
Rosidae, eurosids I, Fabales, Fabaceae, Papilionoideae, Trifolieae,
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EST509456 HOGA Medicago truncatula cDNA clone pHOGA-18E5 5' end,
  'note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
                                                                                                                                                                                                                   1241 CCTTACACATGAACAAGATGGAGAGAGAGAGATTCTGGTGGCTGCATTTTCGGACTTTG 1300
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Hahn,M.G., Ojanen-Reuhs,T., Samac,D., Town,C.D., Van Aken,S., Utterback,T., Cho,J. and Fraser,C.M.
ESTS from roots of Medicago truncatula treated with Oliopalacturonides of DP 6-20 Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                 GTCTATGTGATACACCTCTGGACGACGACGACGAGGATTGATCTTGACGGGA
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0
                                                                                                                       507;
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220 Riverbend Road, Athens, GA 30602-4712,
                                                                                                                     Score 503.8; DB 10;
Pred. No. 3.6e-82;
0; Mismatches 2;
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Complex Carbohydrate Research Center
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Best Local Similarity 99.6%;
Matches 505; Conservative
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Fax: 706-542-4412
Email: hahn@ccrc.u
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AV558412
AV558412.1 GI:8729838
EST.
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Eukaryotosis thaliana
Eukaryotosi Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermacophyta; Magnoliophyta; eudicotyledons; core eudicots;
Srosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases I to 507)
Asamizu, E., Nakamura; Y., Sato, S. and Tabata, S.
Alarge scale analysis of cDNA in Arabidopsis thaliana; Generation of 12,028 non-redundant expressed sequence tags from normalized and size-selected cDNA libraries

20363093
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Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: aeamizu0kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
Location/Qualifiers
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/strain="Columbia"
/db xref="taxon:3702"
/clone="S099BbD2F"
/clone lib="Arabidopsis thaliana green siliques columbia"
/tissue_type="green siliques"
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                                                                                                                       1506 TTCAGAGCAATGAATAAGCTGNNNNNGATGGCCCTAAAGGTTATTGCCTCAAACCTTAAC 1565
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1066 GAATTGTTCAAGATGATAGACACAGACAACAGCGGAACGATTACTTTTGAAGAGCTCAAA 1125
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// Lab host="WLOLM"
// Note="Wector: pBluescript SK-; Site_1: EcoRI; Site_2: Xholf="Wector: pBluescript SK-; Site_1: EcoRI; Site_2: Xholf="Wector: pBluescript SK-; Site_1: EcoRI; Site_2: Xholf="Wector: pBluescript SK-; Site_1: EcoRI; Site_2: Xholf="Wector: pBluescript SK-; Site_1: EcoRI; Site_2: Xholf="Westagene" and packaged into the Unicap XR vector from Stratagene and packaged using Gigapack III Gold packaging extracts. Plasmids containing cDNA inserts were excised from the recombinant lambda-Zap phage using Ex-assist helper phage and propagated in SOLR cells."

30 a 137 c 210 g 258 t
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                                                                                                                              /db_xref="taxon:3880"
/clone="pHGQA-18E5"
/clone lib="HGGA"
/tissue_type="3 day old seedling roots"
 G391443e TIGR sequence name: WIMCE27TK More available at: www.medicago.org Seq primer: SKmod (CTA gAA CTA gtg gAT CC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             205;
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                                                                                         /organism="Medicago truncatula"
/cultivar="A17"
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Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACC
clade, Panicoideae, Andropogoneae, Zea.
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                                                         GCGGGTTTGAAGAGGTCGGATCTGAACTGATGGAATCAGAATCAAGTCTCTCATGGAT 1185
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Arthur, L.W., Mana, G.H., Vogel, J.M., Whitsitt, M.S., Arthur, L.W., Hanafey, M., Morgante, M. and Tingey, S.V. Maize Mapping Project/DuPont Consensus Sequences for Design Unpublished (2002)
                                                                                                                                                                                         GCGGCTGATATCGACAACAGTGGTACAATAGACTACGGAGAATTCCTAGCAGCAAC 1241
gagrinaritchggangcringangcriganaanagriggaachahaacaringgaagagaganaaaa
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Submitted (25-APR-2002) Maize Mapping Project, University
Missouri, Columbia, MO 65211, USA
Location/Qualifiers
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Pred. No. 4.3e-78;
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                                                                                                                                                                                                                                                                                     1315 GTCGCCGTCGTCCACAGCTGCCACTCCATNNNNTCTTCCATCGGGATCTCAAGCCCGAG 1256
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/noce-weeter: pBluescript SK(-); Site_1: EcoRI; Site_2: XhoI; This library targets genes expressed in dormant tubers. This library was made from sections of dormant tuber, avoiding the buds and epidermis. Tubers were stored for one month post-harvest at 40°C. The tuber was peeled, well away from the surface. Then it was chopped into 1-2 mm cubes and immediately frozen in liquid nitrogen. This library is 191 g 235 t
    EST 30-MAY-2001
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(bases 1 to 814)

van der Hoeven, R., Bezzerides, J., Ewing, E., Cho, J., Chlemingo, A., Generations of ESTs from dormant potato tubers

Unpublished (2001)
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                                                                                                                                                                                                                                                                                                                                                             Contact: Cathy Ronning
The Institute for Genomic Research
For clone info: please contact Research Genetics, Libraries
Division tel 1-800-711-6195, email cdna@resgen.com
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BG887873 11near E
EST513724 cSTD Solanum tuberosum cDNA clone cSTD7P13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Solanum tuberosum"
/cultivar="Kennebec"
/db_xref="taxon:4113"
/clone_lib="cSTD713"
/tissuc_type="dormant tuber"
/dev stage="none month post-harvest"
/lab_host="SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                    BG887873.1 GI:14264959
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Matches 597; Conservative
                                                                                                                                       potato.
Solanum tuberosum
                                           mRNA sequence.
BG887873
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Ecker,J.
BAC End Sequences at ATGC
Transhlished (1997)
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B11596.1 GI:2092717
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Fax: 215-898-8780
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Best Local Simi
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Venter, J.C.
Venter, J.C.
Venter, J.C.
Venter, J.C.
Arabidopsis Genomic Sequence Database To Identify Minimal Overlaps for Arabidopsis Genomic Sequencing
Unpublished (1997)
Other GSSs: TBA20TR
Contact: Steve Rounsley
Contact: Steve Rounsley
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0208
Fax: 301 838 0208
Email: rounsley@tigr.org
Seq primer: Ml3-21
Class: BAC ends
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TBA20TFB TAMU Arabidopsis thaliana genomic clone T8A20, DNA
sequence.
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosidas II; Braesicales; Brassicaceae; Arabidopsis.
1 (bases I to 493)
Rounsley, S.D., Kelley, J.M., Field, C.E., Craven, M.B., Adams, M.D. and
                                                                                                                                                                                       978 GCAGTITICICAAATGAATAAGATTAAGAAAATGGCATTACGGGTAATTGCTGAGAGACT 1037
                                                                                                                                                                                                                                                                                                                               1158 GGAATCAGAAATCAAGTCTCTCATGGATGCGGCTGATATCGACAACAGTGGTACAATAGA 1217
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                                                   858 GCTCGAAAGGAGCCCCCAAGAAACGCATTTCTGCTCATGAAGCCTTGTGTCACCCATGGAT 917
                                                                                   421 gercaccadogarectadoscadoarraaccocoárcaaorreraroraciderectoros 480
                                                                                                                      TGTCGATGAACAAGCAGCACCAGACAAGCCTCTTGATCCCAGCAGTCTTATCTCGTCTAAA
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Location/Qualifiers
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/db xref="taxon:3702"
/clone="Taxon"
/clone lib="TANU"
/sex="hermaphrodite"
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B28263.1 GI:2514229
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B28263/c
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TBAZO-T7 TAMU Arabidopsis thaliana genomic clone T8A20, DNA
sequence.
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Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta;
Spermatophyta, Magnoliophyta; eudicotyledons; core eudicots;
Rosidae, eurosidas II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 1087)
1 (bases 1 to 1087)
1 (bases 1 to 1087)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 378 GGAGGTTTGTGAAGGTGGTGAGCTTTTTGATCGGATTGTTTCTAAAGGTCATTTTAGTGA 437
                                                                                                                                                                                                                  GCCAAACCCTAGACGTCCTTCAAACACAGTTCTACCATATCAAACACCACGATTAAGAGA 137
                                                                                                                                                                                                                                                      138 TCATTACCTTCTGGGAAAAAGCTAGGCCAAGGCCAATTTGGAACAACTATCTCTGCAC 197
                                                                                                                                                                                                                                                                                                                                                                                                                                        198 AGAGAAATCAACCTCCGCTAATTACGCCTGCAAATCGATCCCGAAGCGAAAGCTCGTGTG 257
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                                                  Gaps
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University of Pennsylvania
Dept. of Biology, University of Pennsylvania, Philadelphia,
19104
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Length 493;
                                                     Indels
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High quality sequence stop: 873.
Location/Qualifiers
1. 1.087
/organism="Arabidopsis thaliana"
/strain="Columbia"
25.1%; Score 439; DB 17;
ilarity 100.0%; Pred. No. 2.4e-70;
Conservative 0; Mismatches 0;
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Seg primer: T7
Class: BAC ends
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BG596613
BG596613.1 GI:13614753
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Matches 480; Conserv
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I (bases 1 to 528)

Chen, J., Momiyama, M., Chan, E., Mooney, M., Carroon, B., Gilliland, D., Wang, X., Hillman, J., Gualer, K., Kim, C., Doyle, M., Brzoska, P., Ran, X., Hillman, D., Griffin, J., Mouanoutoua, M., Nguyen, D., Tan, R., Rose, M., Burren, B., Ton, B., Kastury, K., Borillo, C., Carpio, T., Policky, J., Suzuki, G., Argentine, C., Shah, S., Nobriga, A., Murry, L., Turner, C., Krikorian, S., Elder, L. and Hanson, D.

Arabidopsis thaliana Gene Expression MicroArray
Contact: David Smoller, Ph.D.
Genome Systems, Inc., a wholly owned subsidiary of Incyte Pharmaceuticals, Inc.

4633 World Parkway Circle, St. Louis, MO 63134, USA
/db_xref="taxon:3702"
/clone="TBA20"
/clone lib="TAMU"
/sex="hermaphodite"
/note="Vector: BeloBACII; Site_1: HindIII; Site_2: HindIII
; Produced by Rod Wing"
a 206 c 178 g 392 t 3 others
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Pred. No. 3.1e-70;
0; Mismatches 7;
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Matches 442; Conservative
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EST495291 cSTS Solanum tuberosum cDNA clone cSTS15M13 5' sequence,
mRNA sequence.
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Solanum tuberosum

Bukariday,

Solanum tuberosum

Bukariday,

Spermarcophyta; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermarcophyta; Magnoliophyta; eudicotyledons; core eudicots;

Asteridae; euasterida I; Solanales; Solanaceae; Solanum.

(bases 1 to 742)

van der Hoeven, R., Bezzerides, J., Sun, H., Cho, J., Chiemingo, A.,

Generations of ESTs from sprouting potato eyes

Unpublished (2000)

Contact: Cathy Ronning
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                                                                                                                                                                                                                                                                                                                                                                                24.3%; Score 424.8; DB 9;
ilarity 92.3%; Pred. No. 9.1e-68;
Conservative 0; Mismatches 37;
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                                                                                                                                                                                                                                                   /note="Vector: pBluescript SK(-); Site 1: BcoRI; Site 2: XhoI; Various sizes of sprouting eyes (Zmm to 15mm) were taken from tubers. The tubers were incubated at 26C in the dark for 2-3 weeks prior to sprouting. The eyes were frozen in liquid nitrogen immediately upon removal from tubers."
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                       Libraries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                           Length 742;
   The Institute for Genomic Research Por clone info: please contact Research Genetics, I Division tel 1-800-711-6195, email cdna@resgen.com seq primer: M13F-R.
                                                                                                                           cultivar="Kennebec"

(db xref="taxon:4113"

(clone="cSTS18M13"

(clone="1b="cSTS"

fissue type="sprouting eyes from tubers"

(dev stage="12-14 weeks post harvest"

lab_host="SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                           Score 418; DB 12; Length 7.
Pred. No. 1.4e-66;
0; Mismatches 185; Indels
                                                                                                               /organism="Solanum tuberosum<sup>:</sup>
                                                                                                                                                                                                                                                                                                                                                                        219 t
                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                        181 9
                                                                                                                                                                                                                                                                                                                                                                                                                             tch 23.9%; al Similarity 74.1%; 529; Conservative (
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Best Local S:
Matches 529
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1 (bases 1 to 813)
VandenBosch, K., Endre, G., Hur, J., Beremand, P., Town, C.D., Van Aken
VandenBosch, K., Cheung, F., Tsai, J. and Fraser, C.M.
ESTs from roots of Medicago truncatula 48 hr after inoculation with
Sinorhizobium meliloti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7
EST 04-MAR-2002
                                                                                                                                                                                                                            Eukaryora; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Vector: pBluescript SK -; site 1: EcoR1; Site 2: Xho1; cDNA was prepared from polyA+ enriched RNA. The colph was directionally ligated into the Unizap XR vector from Strategene and packaged using Gagapack III Gold packaging extracts. Plasmids containing cDNA inserts were excised from the recombinant lambda-Zap phage using its consist helper phage and propagated in SOLR cells."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: kvandenb@cbs.umn.edu
TIGR sequence name: MTABK54TK More information is available at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        166 CAAGGCCAATTTGGAACAACCTATCTCTGCACAGAAATCAACTCCGCTAATTACGCC 225
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 91 GITCICCCTIATGIAACIGAAAICTICGIGAAGITIACACCTIAGGCAGAAACTGGGT 150
BM779035
EST589610 KV2 Medicago truncatula cDNA clone pKV2-22111, mRNA
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Pred. No. 9.7e-64;
); Mismatches 186; Indels 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (2002)
Contact: VandenBosch K
Department of Plant Biology
University of Minnesota
220 Biosci Center, 1445 Gortner Ave, St. Paul, MN
Tel: 612 624 2755
Fax: 612 625 1735
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          www.medicago.org
Seq primer: SKmod (CTA gAA CTA gtg gAT CC)
Location/Qualifiers
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74.0%; Pred
tive 0; I
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BI178776 686 bp mRNA linear EST 09-JUL-2001
ESTS19721 CSTE Solanum tuberosum CDNA Clone CSTEISP12 5' sequence,
mRNA sequence.
BI178776
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Solanum tuberosum

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum.

1 (bases 1 to 686)
van der Hoeven, R., Bezzerides, J., Bachem, C., Visser, R., Cho, J.,
Chiemingo, A., Bougri, O., Buell, C.R., Ronning, C., Tanksley, S. and
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/clone=".cSTE15512"
/clone=1be="cSTE18512"
/tissue_type="axillary buds of stem explants; growing
sink-tuberse"
                                                                                    465
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Generation of ESTs from in vitro grown microtubers Unpublished (2001)
Contact: Cathy Ronning
For institute for Genomic Research
For clone info: please contact Research Genetics, Libraries Division tel 1-800-711-6195, email cdna@resgen.com
Seq primer: M13F-R.
                                                                                                                                                                                                                                                                                                                                                                                                        TIGICIGITITITIACAAGCCAGGIGAAATCTITIAGIGAIGITGTIGGAAGCCCATACTAT
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TATGAAGATTCGGTGTTTGTTCATATTGGAGGTTTGTGAAGGTGGGGGGCTTTTT
                                         TACGAGGATTCGTTTTCTGTTCATTTGGTTATGGAGCTTTGTGAAGGTGGGGAATTGTTT
                                                                                    GATOGGATTGTTTCTAAAGGTCATTTTAGTGAGCGTGAAGCTGTCAAGCTTATTAAGACG
                                                                                                                                GATAGGATTGTGCAGAAAGGGCATTATAGTGAGAGACAAGCTGCTAAGTTGATTAGAACT
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/lab_host="SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Solanum tuberosum"
/cultivar="Bintje"
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1. 686
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BI178776
LOCUS
DEFINITION
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KEYWORDS
SOURCE
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/note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
Xhoj Tissue supplied by Christian Bachem and Richard
Visser (Department of Plant Breeding, Wageningen
University. The Netherlands). The CSTA libraries will
attempt to capture the induction and initiation/initial
growth of the tuber in an in vitro system as described in
Bachem et al. (Plant Journal, 1996). Small microtubers
develop from axillary buds attached to stem explants when
placed on a high sucrose medium (10%). Visible
morphological changes occur synchronously at day five in
the axillary buds. The first library, cSTA (1-20) consists
of axillary buds harvested on days 1-3. This targets
those genes involved in induction of the microtubers. The
following libraries, cSTA (21-40) and cSTA (41-60),
capture genes involved in tuber initiation and outgrowth.
This library is noted as P3 in Tanksley lab notebooks."
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RESULT 15

586

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/lab_host=""CG_ABODI lettuce salinas"
/lab_host="E.cGli"
/lab_host="E.cGli"
/lab_host="E.cGli"
/lab_host="CG_ABODI lettuce salinas"
/lab_host="Year parcons of RNA from a single genotype.
Separate cDNAs were generated using primers that
incorporated unique 5' and 3' tags to distinguish each
source of RNA. cDNAs were then pooled, size-fractionated,
directionally cloned into a custom medium-copy vector and
transformations made with four size classes to minimize
size bias. Details of each source of RNA and library
construction can be obtained at http://cgpdb.ucdavis.edu/
TAG_LIB=QG_ABCDI lettuce salinas
TAG_LISCG_CGGG"
TAG_LISCG_CGGG"
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Kozik, A., Michelmore, R.W., Knapp, S., Matvienko, M., Rieseberg, L.,
Lin, H., van Damme, M., Lavelle, D., Chevalier, P., Ziegle, J., Ellison
, P., Kolkman, J., Slabaugh, M.S., Livingston, K., Zhou, Y., Lai, Z.,
Church, S., Jackson, L. and Bradford, K.
Lettuce and Sunflower ESTs from the Compositae Genome Project
                                                                                                                                             Lactuca sativa.
Lactuca sativa astiva
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids II; Asterales; Asteraceae; Lactuceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Alexander Kozik [R.W.Michelmore]
Contact: Alexander Kozik [R.W.Michelmore Lab
Department of Vegetable Crops, R.W.Michelmore Lab
University of California at Davis (UCD)
Asmundson Hall, UCD, Davis, CA 95616, USA
Tel: 1-(530)-742-1742
Fax: 1-(530)-752-9659
Email: akozik@atgc.org [michelmore@vegmail.ucdavis.edu]
belongs to contig QG_CA_Contig3691, see http://cgpdb.ucdavis.edu/
for details.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'organism="Lactuca sativa"
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Unpublished (2002)
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db_xref="taxon:4236"
clone="QGC5A16"
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